

SEQUENCE LISTING

<110> Jaworski, Jan G.
Blacklock, Brenda J.

<120> FATTY ACID ELONGASE 3-KETOACYL COA
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<151> 2000-06-08

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Ala Ser Arg Leu Thr Ile Asn Asp Leu His Asn Phe Leu Ser Tyr Leu	
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Gln His Asn Leu Ile Thr Val Thr Leu Leu Phe Ala Phe Thr Val Phe	
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Lys	Asn	Thr	Tyr	Ala	Leu	Val	Val	Ser	Thr	Glu	Asn	Ile	Thr	Gln	Gly		
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Ile	Tyr	Ala	Gly	Glu	Asn	Arg	Ser	Met	Met	Val	Ser	Asn	Cys	Leu	Phe		
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Ala	Asp	Asp	Lys	Ser	Phe	Arg	Cys	Val	Gln	Gln	Glu	Asp	Asp	Glu	Ser		
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Thr	Thr	Leu	Thr	Lys	Asn	Ile	Ala	Thr	Leu	Gly	Pro	Leu	Ile	Leu	Pro		

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 Ser Thr Leu His Arg Phe Gly Asn Thr Ser Ser Ser Ser Ile Trp Tyr
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 Glu Leu Ala Tyr Ile Glu Ala Lys Gly Arg Met Lys Lys Gly Asn Lys
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 Trp Val Ala Leu Arg Asn Val Lys Ala Ser Ala Asn Ser Pro Trp Gln
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Leu Phe Asn Leu Cys Phe Phe Pro Leu Thr Ala Ile Val Ala Gly Lys
20 25 30

gcc tat cgg ctt acc ata gac gat ctt cac cac tta tac tat tcc tat 144
Ala Tyr Arg Leu Thr Ile Asp Asp Leu His His Leu Tyr Tyr Ser Tyr
35 40 45

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Leu Gln His Asn Leu Ile Thr Ile Ala Pro Leu Phe Ala Phe Thr Val
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Phe Gly Ser Val Leu Tyr Ile Ala Thr Arg Pro Lys Pro Val Tyr Leu
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Val Glu Tyr Ser Cys Tyr Leu Pro Pro Thr His Cys Arg Ser Ser Ile
85 90 95

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Ser Lys Val Met Asp Ile Phe Tyr Gln Val Arg Lys Ala Asp Pro Ser
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Leu Leu Gln Val Pro Pro Arg Lys Thr Phe Ala Ala Ala Arg Glu Glu
145 150 155 160

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Thr Glu Gln Val Ile Ile Gly Ala Leu Glu Asn Leu Phe Lys Asn Thr
165 170 175

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Asn Val Asn Pro Lys Asp Ile Gly Ile Leu Val Val Asn Ser Ser Met	
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Ala Asp Gly Lys Ser Phe Arg Cys Val Gln Gln Gly Asp Asp Glu Asn	
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Gly Lys Ile Gly Val Ser Leu Ser Lys Asp Ile Thr Asp Val Ala Gly	
325 330 335	
cga acg gtt aag aaa aac ata gca acg ttg ggt ccg ttg att ctt ccg	1056
Arg Thr Val Lys Lys Asn Ile Ala Thr Leu Gly Pro Leu Ile Leu Pro	
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Leu Ser Glu Lys Leu Leu Phe Phe Val Thr Phe Met Gly Lys Lys Leu	
355 360 365	
ttc aaa gat aaa atc aaa cat tac tac gtc ccg gat ttc aaa ctt gct	1152
Phe Lys Asp Lys Ile Lys His Tyr Tyr Val Pro Asp Phe Lys Leu Ala	
370 375 380	
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Ile Asp His Phe Cys Ile His Ala Gly Gly Arg Ala Val Ile Asp Val	
385 390 395 400	
cta gag aag aac cta gcc cta gca ccg atc gat gta gag gca tca aga	1248

Leu Glu Lys Asn Leu Ala Leu Ala Pro Ile Asp Val Glu Ala Ser Arg
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 Ser Thr Leu His Arg Phe Gly Asn Thr Ser Ser Ser Ser Ile Trp Tyr
 420 425 430

gag ttg gca tac ata gaa gca aaa gga agg atg aag aaa ggt aat aaa 1344
 Glu Leu Ala Tyr Ile Glu Ala Lys Gly Arg Met Lys Lys Gly Asn Lys
 435 440 445

gtt tgg cag att gct tta ggg tca ggc ttt aag tgt aac agt gca gtt 1392
 Val Trp Gln Ile Ala Leu Gly Ser Gly Phe Lys Cys Asn Ser Ala Val
 450 455 460

tgg gtg gct cta aac aat gtc aaa gct tgc aca aat agt cct tgg gaa 1440
 Trp Val Ala Leu Asn Asn Val Lys Ala Ser Thr Asn Ser Pro Trp Glu
 465 470 475 480

cac tgc atc gac aga tac ccg gtc aaa att gat tct gat tca ggt aag 1488
 His Cys Ile Asp Arg Tyr Pro Val Lys Ile Asp Ser Asp Ser Gly Lys
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<213> Brassica napus

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 Ala Tyr Arg Leu Thr Ile Asp Asp Leu His His Leu Tyr Tyr Ser Tyr
 35 40 45
 Leu Gln His Asn Leu Ile Thr Ile Ala Pro Leu Phe Ala Phe Thr Val
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 Phe Gly Ser Val Leu Tyr Ile Ala Thr Arg Pro Lys Pro Val Tyr Leu
 65 70 75 80
 Val Glu Tyr Ser Cys Tyr Leu Pro Pro Thr His Cys Arg Ser Ser Ile
 85 90 95
 Ser Lys Val Met Asp Ile Phe Tyr Gln Val Arg Lys Ala Asp Pro Ser
 100 105 110
 Arg Asn Gly Thr Cys Asp Asp Ser Ser Trp Leu Asp Phe Leu Arg Lys
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 Ile Gln Glu Arg Ser Gly Leu Gly Asp Glu Thr His Gly Pro Glu Gly
 130 135 140
 Leu Leu Gln Val Pro Pro Arg Lys Thr Phe Ala Ala Ala Arg Glu Glu
 145 150 155 160
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acg gcg atc gtc gcc gga aaa gcc tat ctt acc ata gac gat ctt cac	207
Thr Ala Ile Val Ala Gly Lys Ala Tyr Leu Thr Ile Asp Asp Leu His	
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His Leu Tyr Tyr Ser Tyr Leu Gln His Asn Leu Ile Thr Ile Ala Pro	
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Leu Leu Ala Phe Thr Val Phe Gly Ser Val Leu Tyr Ile Ala Thr Arg	
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ccc aaa ccg gtt tac ctc gtg gag tac tca tgc tac ctt cca cca acg	351
Pro Lys Pro Val Tyr Leu Val Glu Tyr Ser Cys Tyr Leu Pro Pro Thr	
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cat tgt aga tca agt atc tcc aag gtc atg gat atc ttt ttc caa gta	399
His Cys Arg Ser Ser Ile Ser Lys Val Met Asp Ile Phe Phe Gln Val	
90 95 100 105	
aga aaa gct gat cct tct cgg aac ggc acg tgc gat gac tcg tcc tgg	447
Arg Lys Ala Asp Pro Ser Arg Asn Gly Thr Cys Asp Asp Ser Ser Trp	
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ctt gac ttc ttg agg aag att caa gaa cgt tca ggt cta ggc gat gaa	495
Leu Asp Phe Leu Arg Lys Ile Gln Glu Arg Ser Gly Leu Gly Asp Glu	
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acc cac ggg ccc gag ggg ctg ctt cag gtc cct ccc cgg aag act ttt	543
Thr His Gly Pro Glu Gly Leu Gln Val Pro Pro Arg Lys Thr Phe	
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gcg cgc gcg cgt gaa gag acg gag caa gtt atc att ggt gcg cta gaa	591
Ala Arg Ala Arg Glu Glu Thr Glu Gln Val Ile Ile Gly Ala Leu Glu	
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aat cta ttc aag aac acc aat gtt aac cct aaa gat ata ggt ata ctt	639
Asn Leu Phe Lys Asn Thr Asn Val Asn Pro Lys Asp Ile Gly Ile Leu	
170 175 180 185	
gtg gtg aac tca agc atg ttt aat cca act cct tcg ctc tcc gcg atg	687
Val Val Asn Ser Ser Met Phe Asn Pro Thr Pro Ser Leu Ser Ala Met	
190 195 200	
gtc gtt aac act ttc aag ctc cga agc aac gta aga agc ttt aac ctt	735
Val Val Asn Thr Phe Lys Leu Arg Ser Asn Val Arg Ser Phe Asn Leu	
205 210 215	
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Gly Gly Met Gly Cys Ser Ala Gly Val Ile Ala Ile Asp Leu Ala Lys	
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gac ttg ttg cat gtc cat aaa aat acg tat gct ctt gtg gtg agc aca	831

Asp	Leu	Leu	His	Val	His	Lys	Asn	Thr	Tyr	Ala	Leu	Val	Val	Ser	Thr		
235						240					245						
gag	aac	atc	act	tat	aac	att	tac	gct	ggc	gat	aat	agg	tcc	atg	atg	879	
Glu	Asn	Ile	Thr	Tyr	Asn	Ile	Tyr	Ala	Gly	Asp	Asn	Arg	Ser	Met	Met		
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Val	Ser	Asn	Cys	Leu	Phe	Arg	Val	Gly	Gly	Ala	Ile	Leu	Leu	Ser			
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Asn	Lys	Pro	Arg	Asp	Arg	Arg	Arg	Ser	Lys	Tyr	Glu	Leu	Val	His	Thr		
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Val	Arg	Thr	His	Thr	Gly	Ala	Asp	Asp	Lys	Ser	Phe	Arg	Cys	Val	Gln		
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caa	gga	gac	gat	gag	aac	ggc	caa	acc	gga	gtg	agt	ttg	tcc	aag	gac	1071	
Gln	Gly	Asp	Asp	Glu	Asn	Gly	Gln	Thr	Gly	Val	Ser	Leu	Ser	Lys	Asp		
			315			320						325					
ata	acc	gat	ggt	gct	ggc	cga	acg	ggt	aag	aaa	aac	ata	gca	acg	ctg	1119	
Ile	Thr	Asp	Val	Ala	Gly	Arg	Thr	Val	Lys	Lys	Asn	Ile	Ala	Thr	Leu		
330					335					340					345		
ggc	ccg	ttg	att	ctt	ccg	tta	agc	gag	aaa	ctt	ctt	ttt	ttc	ggt	acc	1167	
Gly	Pro	Leu	Ile	Leu	Pro	Leu	Ser	Glu	Lys	Leu	Leu	Phe	Phe	Val	Thr		
				350					355					360			
ttc	atg	ggc	aag	aaa	ctt	ttc	aaa	gac	gaa	atc	aaa	cat	tat	tac	gtc	1215	
Phe	Met	Gly	Lys	Lys	Leu	Phe	Lys	Asp	Glu	Ile	Lys	His	Tyr	Tyr	Val		
			365					370					375				
ccg	gac	ttc	aag	ctt	gct	atc	gac	cat	ttt	tgt	ata	cat	gcc	gga	ggc	1263	
Pro	Asp	Phe	Lys	Leu	Ala	Ile	Asp	His	Phe	Cys	Ile	His	Ala	Gly	Gly		
			380				385						390				
aaa	gcc	gtg	att	gat	gtg	cta	gag	aag	aac	cta	ggc	cta	gca	ccg	atc	1311	
Lys	Ala	Val	Ile	Asp	Val	Leu	Glu	Lys	Asn	Leu	Gly	Leu	Ala	Pro	Ile		
			395			400					405						
gat	gta	gag	gca	tca	aga	tca	acg	tta	cat	aga	ttt	gga	aac	act	tca	1359	
Asp	Val	Glu	Ala	Ser	Arg	Ser	Thr	Leu	His	Arg	Phe	Gly	Asn	Thr	Ser		
410					415					420					425		
tct	agc	tca	ata	tgg	tat	gag	ttg	gca	tac	ata	gaa	ccc	aaa	gga	agg	1407	
Ser	Ser	Ser	Ile	Trp	Tyr	Glu	Leu	Ala	Tyr	Ile	Glu	Pro	Lys	Gly	Arg		
				430					435					440			
atg	aag	aaa	ggc	aat	aaa	gtt	tgg	cag	att	gct	tta	ggg	tca	ggc	ttt	1455	
Met	Lys	Lys	Gly	Asn	Lys	Val	Trp	Gln	Ile	Ala	Leu	Gly	Ser	Gly	Phe		
			445					450					455				
aag	tgt	aac	agt	gca	gtt	tgg	gtg	gct	cta	aac	aat	gtc	aaa	gct	tca	1503	
Lys	Cys	Asn	Ser	Ala	Val	Trp	Val	Ala	Leu	Asn	Asn	Val	Lys	Ala	Ser		

460 465 470

aca aat agt cct tgg gaa cac tgc atc gac aga tac ccg gtt aaa att 1551
 Thr Asn Ser Pro Trp Glu His Cys Ile Asp Arg Tyr Pro Val Lys Ile
 475 480 485

gat tct gat tca ggt aag tca gag act cgt gtc cca aac ggt cgg tcc 1599
 Asp Ser Asp Ser Gly Lys Ser Glu Thr Arg Val Pro Asn Gly Arg Ser
 490 495 500 505

taataaatga tgtttgctct ctttcgtttc tttttattgg ttataataat ttgatggcca 1659
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 Gln His Asn Leu Ile Thr Ile Ala Pro Leu Leu Ala Phe Thr Val Phe
 50 55 60
 Gly Ser Val Leu Tyr Ile Ala Thr Arg Pro Lys Pro Val Tyr Leu Val
 65 70 75 80
 Glu Tyr Ser Cys Tyr Leu Pro Pro Thr His Cys Arg Ser Ser Ile Ser
 85 90 95
 Lys Val Met Asp Ile Phe Phe Gln Val Arg Lys Ala Asp Pro Ser Arg
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 115 120 125
 Gln Glu Arg Ser Gly Leu Gly Asp Glu Thr His Gly Pro Glu Gly Leu
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 Leu Gln Val Pro Pro Arg Lys Thr Phe Ala Arg Ala Arg Glu Glu Thr
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 Glu Gln Val Ile Ile Gly Ala Leu Glu Asn Leu Phe Lys Asn Thr Asn
 165 170 175
 Val Asn Pro Lys Asp Ile Gly Ile Leu Val Val Asn Ser Ser Met Phe
 180 185 190
 Asn Pro Thr Pro Ser Leu Ser Ala Met Val Val Asn Thr Phe Lys Leu
 195 200 205
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 210 215 220
 Gly Val Ile Ala Ile Asp Leu Ala Lys Asp Leu Leu His Val His Lys
 225 230 235 240
 Asn Thr Tyr Ala Leu Val Val Ser Thr Glu Asn Ile Thr Tyr Asn Ile
 245 250 255
 Tyr Ala Gly Asp Asn Arg Ser Met Met Val Ser Asn Cys Leu Phe Arg
 260 265 270
 Val Gly Gly Ala Ala Ile Leu Leu Ser Asn Lys Pro Arg Asp Arg Arg
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Thr Val Lys Lys Asn Ile Ala Thr Leu Gly Pro Leu Ile Leu Pro Leu
              340              345              350
Ser Glu Lys Leu Leu Phe Phe Val Thr Phe Met Gly Lys Lys Leu Phe
              355              360              365
Lys Asp Glu Ile Lys His Tyr Tyr Val Pro Asp Phe Lys Leu Ala Ile
              370              375              380
Asp His Phe Cys Ile His Ala Gly Gly Lys Ala Val Ile Asp Val Leu
385              390              395              400
Glu Lys Asn Leu Gly Leu Ala Pro Ile Asp Val Glu Ala Ser Arg Ser
              405              410              415
Thr Leu His Arg Phe Gly Asn Thr Ser Ser Ser Ile Trp Tyr Glu
              420              425              430
Leu Ala Tyr Ile Glu Pro Lys Gly Arg Met Lys Lys Gly Asn Lys Val
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Trp Gln Ile Ala Leu Gly Ser Gly Phe Lys Cys Asn Ser Ala Val Trp
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Val Ala Leu Asn Asn Val Lys Ala Ser Thr Asn Ser Pro Trp Glu His
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3' 1179 bp from B. napus elongase KCS (SEQ ID
NO:3); designated At114

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ttt ttc aac ctc tgt ttg ttc ccg tta acg gcg ttc ctc gcc gga aaa      96
Phe Phe Asn Leu Cys Leu Phe Pro Leu Thr Ala Phe Leu Ala Gly Lys
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gcc tct cgg ctt acc ata aac gat ctc cac aac ttc ctt tcc tat ctc      144
Ala Ser Arg Leu Thr Ile Asn Asp Leu His Asn Phe Leu Ser Tyr Leu
      35              40              45

caa cac aac ctt ata aca gta act tta ctc ttt gct ttc act gtt ttc      192
Gln His Asn Leu Ile Thr Val Thr Leu Leu Phe Ala Phe Thr Val Phe
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gac tac tcg tgt tac ctt ccg cca ccg cat ctc aaa gtt agt gtc tct	288
Asp Tyr Ser Cys Tyr Leu Pro Pro Pro His Leu Lys Val Ser Val Ser	
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aaa gtc atg gat att ttc tac caa ata aga aaa gct gat act tct tca	336
Lys Val Met Asp Ile Phe Tyr Gln Ile Arg Lys Ala Asp Thr Ser Ser	
100 105 110	
cgg aac ggc acg tgt gat gat tcg tcg tgg ctt gac ttc ttg agg aag	384
Arg Asn Gly Thr Cys Asp Asp Ser Ser Trp Leu Asp Phe Leu Arg Lys	
115 120 125	
att caa gaa cgt tca ggt cta ggc gat gaa act cac ggg ccc gag ggg	432
Ile Gln Glu Arg Ser Gly Leu Gly Asp Glu Thr His Gly Pro Glu Gly	
130 135 140	
ctg ctt cag gtc cct ccc cgg aag act ttt gcg gcg gcg cgt gaa gag	480
Leu Leu Gln Val Pro Pro Arg Lys Thr Phe Ala Ala Ala Arg Glu Glu	
145 150 155 160	
acg gag caa gtt atc att ggt gcg cta gaa aat cta ttc aag aac acc	528
Thr Glu Gln Val Ile Ile Gly Ala Leu Glu Asn Leu Phe Lys Asn Thr	
165 170 175	
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Asn Val Asn Pro Lys Asp Ile Gly Ile Leu Val Val Asn Ser Ser Met	
180 185 190	
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Phe Asn Pro Thr Pro Ser Leu Ser Ala Met Val Val Asn Thr Phe Lys	
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Leu Arg Ser Asn Val Arg Ser Phe Asn Leu Gly Gly Met Gly Cys Ser	
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Ala Gly Val Ile Ala Ile Asp Leu Ala Lys Asp Leu Leu His Val His	
225 230 235 240	
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Lys Asn Thr Tyr Ala Leu Val Val Ser Thr Glu Asn Ile Thr Tyr Asn	
245 250 255	
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Ile Tyr Ala Gly Asp Asn Arg Ser Met Met Val Ser Asn Cys Leu Phe	
260 265 270	
cgt gtt ggt ggg gcc gct att ttg ctc tcc aac aag cct gga gat cgt	864
Arg Val Gly Gly Ala Ala Ile Leu Leu Ser Asn Lys Pro Gly Asp Arg	
275 280 285	

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 290 295 300

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 325 330 335

cga acg gtt aag aaa aac ata gca acg ttg ggt ccg ttg att ctt ccg 1056
 Arg Thr Val Lys Lys Asn Ile Ala Thr Leu Gly Pro Leu Ile Leu Pro
 340 345 350

tta agc gag aaa ctt ctt ttt ttc gtt acc ttc atg ggc aag aaa ctt 1104
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 355 360 365

ttc aaa gat aaa atc aaa cat tac tac gtc ccg gat ttc aaa ctt gct 1152
 Phe Lys Asp Lys Ile Lys His Tyr Tyr Val Pro Asp Phe Lys Leu Ala
 370 375 380

att gac cat ttt tgt ata cat gcc gga ggc aga gcc gtg att gat gtg 1200
 Ile Asp His Phe Cys Ile His Ala Gly Gly Arg Ala Val Ile Asp Val
 385 390 395 400

cta gag aag aac cta gcc cta gca ccg atc gat gta gag gca tca aga 1248
 Leu Glu Lys Asn Leu Ala Leu Ala Pro Ile Asp Val Glu Ala Ser Arg
 405 410 415

tca acg tta cat aga ttt gga aac act tca tct agc tca ata tgg tat 1296
 Ser Thr Leu His Arg Phe Gly Asn Thr Ser Ser Ser Ser Ile Trp Tyr
 420 425 430

gag ttg gca tac ata gaa rca aaa gga agg atg aag aaa ggt aat aaa 1344
 Glu Leu Ala Tyr Ile Glu Xaa Lys Gly Arg Met Lys Lys Gly Asn Lys
 435 440 445

gtt tgg cag att gct tta ggg tca ggc ttt aag tgt aac agt gca gtt 1392
 Val Trp Gln Ile Ala Leu Gly Ser Gly Phe Lys Cys Asn Ser Ala Val
 450 455 460

tgg gtg gct cta aac aat gtc aaa gct tcg aca aat agt cct tgg gaa 1440
 Trp Val Ala Leu Asn Asn Val Lys Ala Ser Thr Asn Ser Pro Trp Glu
 465 470 475 480

cac tgc atc gac aga tac ccg gtc aaa att gat tct gat tca ggt aag 1488
 His Cys Ile Asp Arg Tyr Pro Val Lys Ile Asp Ser Asp Ser Gly Lys
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 Ser Glu Thr Arg Val Pro Asn Gly Arg Ser
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 Ala Ser Arg Leu Thr Ile Asn Asp Leu His Asn Phe Leu Ser Tyr Leu
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 Gln His Asn Leu Ile Thr Val Thr Leu Leu Phe Ala Phe Thr Val Phe
 50 55 60
 Gly Leu Val Leu Tyr Ile Val Thr Arg Pro Asn Pro Val Tyr Leu Val
 65 70 75 80
 Asp Tyr Ser Cys Tyr Leu Pro Pro Pro His Leu Lys Val Ser Val Ser
 85 90 95
 Lys Val Met Asp Ile Phe Tyr Gln Ile Arg Lys Ala Asp Thr Ser Ser
 100 105 110
 Arg Asn Gly Thr Cys Asp Asp Ser Ser Trp Leu Asp Phe Leu Arg Lys
 115 120 125
 Ile Gln Glu Arg Ser Gly Leu Gly Asp Glu Thr His Gly Pro Glu Gly
 130 135 140
 Leu Leu Gln Val Pro Pro Arg Lys Thr Phe Ala Ala Arg Glu Glu
 145 150 155 160
 Thr Glu Gln Val Ile Ile Gly Ala Leu Glu Asn Leu Phe Lys Asn Thr
 165 170 175
 Asn Val Asn Pro Lys Asp Ile Gly Ile Leu Val Val Asn Ser Ser Met
 180 185 190
 Phe Asn Pro Thr Pro Ser Leu Ser Ala Met Val Val Asn Thr Phe Lys
 195 200 205
 Leu Arg Ser Asn Val Arg Ser Phe Asn Leu Gly Gly Met Gly Cys Ser
 210 215 220
 Ala Gly Val Ile Ala Ile Asp Leu Ala Lys Asp Leu Leu His Val His
 225 230 235 240
 Lys Asn Thr Tyr Ala Leu Val Val Ser Thr Glu Asn Ile Thr Tyr Asn
 245 250 255
 Ile Tyr Ala Gly Asp Asn Arg Ser Met Met Val Ser Asn Cys Leu Phe
 260 265 270
 Arg Val Gly Gly Ala Ala Ile Leu Leu Ser Asn Lys Pro Gly Asp Arg
 275 280 285
 Arg Arg Ser Lys Tyr Glu Leu Val His Thr Val Arg Thr His Thr Gly
 290 295 300
 Ala Asp Gly Lys Ser Phe Arg Cys Val Gln Gln Gly Asp Asp Glu Asn
 305 310 315 320
 Gly Lys Ile Gly Val Ser Leu Ser Lys Asp Ile Thr Asp Val Ala Gly
 325 330 335

Arg Thr Val Lys Lys Asn Ile Ala Thr Leu Gly Pro Leu Ile Leu Pro
 340 345 350
 Leu Ser Glu Lys Leu Leu Phe Phe Val Thr Phe Met Gly Lys Lys Leu
 355 360 365
 Phe Lys Asp Lys Ile Lys His Tyr Tyr Val Pro Asp Phe Lys Leu Ala
 370 375 380
 Ile Asp His Phe Cys Ile His Ala Gly Gly Arg Ala Val Ile Asp Val
 385 390 395 400
 Leu Glu Lys Asn Leu Ala Leu Ala Pro Ile Asp Val Glu Ala Ser Arg
 405 410 415
 Ser Thr Leu His Arg Phe Gly Asn Thr Ser Ser Ser Ser Ile Trp Tyr
 420 425 430
 Glu Leu Ala Tyr Ile Glu Xaa Lys Gly Arg Met Lys Lys Gly Asn Lys
 435 440 445
 Val Trp Gln Ile Ala Leu Gly Ser Gly Phe Lys Cys Asn Ser Ala Val
 450 455 460
 Trp Val Ala Leu Asn Asn Val Lys Ala Ser Thr Asn Ser Pro Trp Glu
 465 470 475 480
 His Cys Ile Asp Arg Tyr Pro Val Lys Ile Asp Ser Asp Ser Gly Lys
 485 490 495
 Ser Glu Thr Arg Val Pro Asn Gly Arg Ser
 500 505

<210> 9

<211> 1518

<212> DNA

<213> Artificial Sequence

<220>

<223> 5' 222 bp from A. thaliana FAE1 (SEQ ID NO:1) and
 3' 1296 bp from B. napus elongase KCS (SEQ ID
 NO:3); designated At74

<221> CDS

<222> (1) ... (1515)

<400> 9

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 1 5 10 15

ttt ttc aac ctc tgt ttg ttc ccg tta acg gcg ttc ctc gcc gga aaa 96
 Phe Phe Asn Leu Cys Leu Phe Pro Leu Thr Ala Phe Leu Ala Gly Lys
 20 25 30

gcc tct cgg ctt acc ata aac gat ctc cac aac ttc ctt tcc tat ctc 144
 Ala Ser Arg Leu Thr Ile Asn Asp Leu His Asn Phe Leu Ser Tyr Leu
 35 40 45

caa cac aac ctt ata aca gta act tta ctc ttt gct ttc act gtt ttc 192
 Gln His Asn Leu Ile Thr Val Thr Leu Leu Phe Ala Phe Thr Val Phe
 50 55 60

ggt ttg gtt ctc tac atc gta acc cga ccc aaa ccg gtt tac ctc gtt 240
 Gly Leu Val Leu Tyr Ile Val Thr Arg Pro Lys Pro Val Tyr Leu Val
 65 70 75 80

gag tac tca tgc tac ctt cca cca acg cat tgt aga tca agt atc tcc	288
Glu Tyr Ser Cys Tyr Leu Pro Pro Thr His Cys Arg Ser Ser Ile Ser	
85 90 95	
aag gtc atg gat atc ttt tat caa gta aga aaa gct gat cct tct cgg	336
Lys Val Met Asp Ile Phe Tyr Gln Val Arg Lys Ala Asp Pro Ser Arg	
100 105 110	
aac ggc acg tgc gat gac tcg tcg tgg ctt gac ttc ttg agg aag att	384
Asn Gly Thr Cys Asp Asp Ser Ser Trp Leu Asp Phe Leu Arg Lys Ile	
115 120 125	
caa gaa cgt tca ggt cta ggc gat gaa act cac ggg ccc gag ggg ctg	432
Gln Glu Arg Ser Gly Leu Gly Asp Glu Thr His Gly Pro Glu Gly Leu	
130 135 140	
ctt cag gtc cct ccc cgg aag act ttt gcg gcg gcg cgt gaa gag acg	480
Leu Gln Val Pro Pro Arg Lys Thr Phe Ala Ala Ala Arg Glu Glu Thr	
145 150 155 160	
gag caa gtt atc att ggt gcg cta gaa aat cta ttc aag aac acc aac	528
Glu Gln Val Ile Ile Gly Ala Leu Glu Asn Leu Phe Lys Asn Thr Asn	
165 170 175	
gtt aac cct aaa gat ata ggt ata ctt gtg gtg aac tca agc atg ttt	576
Val Asn Pro Lys Asp Ile Gly Ile Leu Val Val Asn Ser Ser Met Phe	
180 185 190	
aat cca act cca tcg ctc tcc gcg atg gtc gtt aac act ttc aag ctc	624
Asn Pro Thr Pro Ser Leu Ser Ala Met Val Val Asn Thr Phe Lys Leu	
195 200 205	
cga agc aac gta aga agc ttt aac ctt ggt ggc atg ggt tgt agt gcc	672
Arg Ser Asn Val Arg Ser Phe Asn Leu Gly Gly Met Gly Cys Ser Ala	
210 215 220	
ggc gtt ata gcc att gat cta gca aag gac ttg ttg cat gtc cat aaa	720
Gly Val Ile Ala Ile Asp Leu Ala Lys Asp Leu Leu His Val His Lys	
225 230 235 240	
aat acg tat gct ctt gtg gtg agc aca gag aac atc act tat aac att	768
Asn Thr Tyr Ala Leu Val Val Ser Thr Glu Asn Ile Thr Tyr Asn Ile	
245 250 255	
tac gct ggt gat aat agg tcc atg atg gtt tca aat tgc ttg ttc cgt	816
Tyr Ala Gly Asp Asn Arg Ser Met Met Val Ser Asn Cys Leu Phe Arg	
260 265 270	
gtt ggt ggg gcc gct att ttg ctc tcc aac aag cct gga gat cgt aga	864
Val Gly Gly Ala Ala Ile Leu Leu Ser Asn Lys Pro Gly Asp Arg Arg	
275 280 285	
cgg tcc aag tac gag cta gtt cac acg gtt cga acg cat acc gga gct	912
Arg Ser Lys Tyr Glu Leu Val His Thr Val Arg Thr His Thr Gly Ala	
290 295 300	
gac ggc aag tct ttt cgt tgc gtg caa caa gga gac gat gag aac ggc	960

Asp Gly Lys Ser Phe Arg Cys Val Gln Gln Gly Asp Asp Glu Asn Gly	
305 310 315 320	
aaa atc gga gtg agt ttg tcc aag gac ata acc gat gtt gct ggt cga	1008
Lys Ile Gly Val Ser Leu Ser Lys Asp Ile Thr Asp Val Ala Gly Arg	
325 330 335	
acg gtt aag aaa aac ata gca acg ttg ggt ccg ttg att ctt ccg tta	1056
Thr Val Lys Lys Asn Ile Ala Thr Leu Gly Pro Leu Ile Leu Pro Leu	
340 345 350	
agc gag aaa ctt ctt ttt ttc gtt acc ttc atg ggc aag aaa ctt ttc	1104
Ser Glu Lys Leu Leu Phe Phe Val Thr Phe Met Gly Lys Lys Leu Phe	
355 360 365	
aaa gat aaa atc aaa cat tac tac gtc ccg gat ttc aaa ctt gct att	1152
Lys Asp Lys Ile Lys His Tyr Tyr Val Pro Asp Phe Lys Leu Ala Ile	
370 375 380	
gac cat ttt tgt ata cat gcc gga ggc aga gcc gtg att gat gtg cta	1200
Asp His Phe Cys Ile His Ala Gly Gly Arg Ala Val Ile Asp Val Leu	
385 390 395 400	
gag aag aac cta gcc cta gca ccg atc gat gta gag gca tca aga tca	1248
Glu Lys Asn Leu Ala Leu Ala Pro Ile Asp Val Glu Ala Ser Arg Ser	
405 410 415	
acg tta cat aga ttt gga aac act tca tct agc tca ata tgg tat gag	1296
Thr Leu His Arg Phe Gly Asn Thr Ser Ser Ser Ser Ile Trp Tyr Glu	
420 425 430	
ttg gca tac ata gaa gca aaa gga agg atg aag aaa ggt aat aaa gtt	1344
Leu Ala Tyr Ile Glu Ala Lys Gly Arg Met Lys Lys Gly Asn Lys Val	
435 440 445	
tgg cag att gct tta ggg tca ggc ttt aag tgt aac agt gca gtt tgg	1392
Trp Gln Ile Ala Leu Gly Ser Gly Phe Lys Cys Asn Ser Ala Val Trp	
450 455 460	
gtg gct cta aac aat gtc aaa gct tcg aca aat agt cct tgg gaa cac	1440
Val Ala Leu Asn Asn Val Lys Ala Ser Thr Asn Ser Pro Trp Glu His	
465 470 475 480	
tgc atc gac aga tac ccg gtc aaa att gat tct gat tca ggt aag tca	1488
Cys Ile Asp Arg Tyr Pro Val Lys Ile Asp Ser Asp Ser Gly Lys Ser	
485 490 495	
gag act cgt gtc caa aac ggt cgg tcc taa	1518
Glu Thr Arg Val Gln Asn Gly Arg Ser	
500 505	

<210> 10

<211> 505

<212> PRT

<213> Artificial Sequence

<220>

<223> 5' 74 amino acids from *A. thaliana* FAE1 (SEQ ID NO:2) and 3' 431 amino acids from *B. napus* elongase KCS (SEQ ID NO:4); designated At74

<400> 10

Met	Thr	Ser	Val	Asn	Val	Lys	Leu	Leu	Tyr	Arg	Tyr	Val	Leu	Thr	Asn
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Phe	Phe	Asn	Leu	Cys	Leu	Phe	Pro	Leu	Thr	Ala	Phe	Leu	Ala	Gly	Lys
		20						25					30		
Ala	Ser	Arg	Leu	Thr	Ile	Asn	Asp	Leu	His	Asn	Phe	Leu	Ser	Tyr	Leu
		35					40					45			
Gln	His	Asn	Leu	Ile	Thr	Val	Thr	Leu	Leu	Phe	Ala	Phe	Thr	Val	Phe
	50					55				60					
Gly	Leu	Val	Leu	Tyr	Ile	Val	Thr	Arg	Pro	Lys	Pro	Val	Tyr	Leu	Val
65					70					75					80
Glu	Tyr	Ser	Cys	Tyr	Leu	Pro	Pro	Thr	His	Cys	Arg	Ser	Ser	Ile	Ser
			85						90					95	
Lys	Val	Met	Asp	Ile	Phe	Tyr	Gln	Val	Arg	Lys	Ala	Asp	Pro	Ser	Arg
			100					105					110		
Asn	Gly	Thr	Cys	Asp	Asp	Ser	Ser	Trp	Leu	Asp	Phe	Leu	Arg	Lys	Ile
		115					120						125		
Gln	Glu	Arg	Ser	Gly	Leu	Gly	Asp	Glu	Thr	His	Gly	Pro	Glu	Gly	Leu
	130					135					140				
Leu	Gln	Val	Pro	Pro	Arg	Lys	Thr	Phe	Ala	Ala	Ala	Arg	Glu	Glu	Thr
145					150					155					160
Glu	Gln	Val	Ile	Ile	Gly	Ala	Leu	Glu	Asn	Leu	Phe	Lys	Asn	Thr	Asn
			165						170					175	
Val	Asn	Pro	Lys	Asp	Ile	Gly	Ile	Leu	Val	Val	Asn	Ser	Ser	Met	Phe
			180					185					190		
Asn	Pro	Thr	Pro	Ser	Leu	Ser	Ala	Met	Val	Val	Asn	Thr	Phe	Lys	Leu
		195					200					205			
Arg	Ser	Asn	Val	Arg	Ser	Phe	Asn	Leu	Gly	Gly	Met	Gly	Cys	Ser	Ala
	210					215						220			
Gly	Val	Ile	Ala	Ile	Asp	Leu	Ala	Lys	Asp	Leu	Leu	His	Val	His	Lys
225					230					235					240
Asn	Thr	Tyr	Ala	Leu	Val	Val	Ser	Thr	Glu	Asn	Ile	Thr	Tyr	Asn	Ile
			245						250					255	
Tyr	Ala	Gly	Asp	Asn	Arg	Ser	Met	Met	Val	Ser	Asn	Cys	Leu	Phe	Arg
			260					265					270		
Val	Gly	Gly	Ala	Ala	Ile	Leu	Leu	Ser	Asn	Lys	Pro	Gly	Asp	Arg	Arg
		275					280					285			
Arg	Ser	Lys	Tyr	Glu	Leu	Val	His	Thr	Val	Arg	Thr	His	Thr	Gly	Ala
	290					295					300				
Asp	Gly	Lys	Ser	Phe	Arg	Cys	Val	Gln	Gln	Gly	Asp	Asp	Glu	Asn	Gly
305					310					315					320
Lys	Ile	Gly	Val	Ser	Leu	Ser	Lys	Asp	Ile	Thr	Asp	Val	Ala	Gly	Arg
			325						330					335	
Thr	Val	Lys	Lys	Asn	Ile	Ala	Thr	Leu	Gly	Pro	Leu	Ile	Leu	Pro	Leu
			340					345					350		
Ser	Glu	Lys	Leu	Leu	Phe	Phe	Val	Thr	Phe	Met	Gly	Lys	Lys	Leu	Phe
		355					360					365			
Lys	Asp	Lys	Ile	Lys	His	Tyr	Val	Pro	Asp	Phe	Lys	Leu	Ala	Ile	
	370					375				380					
Asp	His	Phe	Cys	Ile	His	Ala	Gly	Gly	Arg	Ala	Val	Ile	Asp	Val	Leu
385					390					395					400
Glu	Lys	Asn	Leu	Ala	Leu	Ala	Pro	Ile	Asp	Val	Glu	Ala	Ser	Arg	Ser

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                405                410                415
Thr Leu His Arg Phe Gly Asn Thr Ser Ser Ser Ser Ile Trp Tyr Glu
                420                425                430
Leu Ala Tyr Ile Glu Ala Lys Gly Arg Met Lys Lys Gly Asn Lys Val
                435                440                445
Trp Gln Ile Ala Leu Gly Ser Gly Phe Lys Cys Asn Ser Ala Val Trp
                450                455                460
Val Ala Leu Asn Asn Val Lys Ala Ser Thr Asn Ser Pro Trp Glu His
465                470                475                480
Cys Ile Asp Arg Tyr Pro Val Lys Ile Asp Ser Asp Ser Gly Lys Ser
                485                490                495
Glu Thr Arg Val Gln Asn Gly Arg Ser
                500                505

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<210> 11
<211> 1521
<212> DNA
<213> Artificial Sequence

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<220>
<223> 5' 342 bp from A. thaliana FAE1 (SEQ ID NO:1) and
      3' 1179 bp from B. napus elongase KCS (SEQ ID
      NO:3) having mutations at positions 271, 272 and
      275; designated At114 L91C K92R

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<221> CDS
<222> (1)...(1518)

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<400> 11
atg acg tcc gtt aac gtt aag ctc ctt tac cgt tat gtc tta acc aac      48
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  1                5                10                15

ttt ttc aac ctc tgt ttg ttc ccg tta acg gcg ttc ctc gcc gga aaa      96
Phe Phe Asn Leu Cys Leu Phe Pro Leu Thr Ala Phe Leu Ala Gly Lys
                20                25                30

gcc tct cgg ctt acc ata aac gat ctc cac aac ttc ctt tcc tat ctc      144
Ala Ser Arg Leu Thr Ile Asn Asp Leu His Asn Phe Leu Ser Tyr Leu
                35                40                45

caa cac aac ctt ata aca gta act tta ctc ttt gct ttc act gtt ttc      192
Gln His Asn Leu Ile Thr Val Thr Leu Leu Phe Ala Phe Thr Val Phe
                50                55                60

ggg ttg gtt ctc tac atc gta acc cga ccc aat ccg gtt tat ctc gtt      240
Gly Leu Val Leu Tyr Ile Val Thr Arg Pro Asn Pro Val Tyr Leu Val
                65                70                75                80

gac tac tcg tgt tac ctt ccg cca ccg cat tgc aga gtt agt gtc tct      288
Asp Tyr Ser Cys Tyr Leu Pro Pro Pro His Cys Arg Val Ser Val Ser
                85                90                95

aaa gtc atg gat att ttc tac caa ata aga aaa gct gat act tct tca      336
Lys Val Met Asp Ile Phe Tyr Gln Ile Arg Lys Ala Asp Thr Ser Ser
                100                105                110

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cgg aac ggc acg tgt gat aat tcg tcg tgg ctt gac ttc ttg agg aag Arg Asn Gly Thr Cys Asp Asn Ser Ser Trp Leu Asp Phe Leu Arg Lys 115 120 125	384
att caa gaa cgt tca ggt cta ggc gat gaa act cac ggg ccc gag ggg Ile Gln Glu Arg Ser Gly Leu Gly Asp Glu Thr His Gly Pro Glu Gly 130 135 140	432
ctg ctt cag gtc cct ccc cgg aag act ttt gcg gcg gcg cgt gaa gag Leu Leu Gln Val Pro Pro Arg Lys Thr Phe Ala Ala Ala Arg Glu Glu 145 150 155 160	480
acg gag caa gtt atc att ggt gcg cta gaa aat cta ttc aag aac acc Thr Glu Gln Val Ile Ile Gly Ala Leu Glu Asn Leu Phe Lys Asn Thr 165 170 175	528
aac gtt aac cct aaa gat ata ggt ata ctt gtg gtg aac tca agc atg Asn Val Asn Pro Lys Asp Ile Gly Ile Leu Val Val Asn Ser Ser Met 180 185 190	576
ttt aat cca act cca tcg ctc tcc gcg atg gtc gtt aac act ttc aag Phe Asn Pro Thr Pro Ser Leu Ser Ala Met Val Val Asn Thr Phe Lys 195 200 205	624
ctc cga agc aac gta aga agc ttt aac ctt ggt ggc atg ggt tgt agt Leu Arg Ser Asn Val Arg Ser Phe Asn Leu Gly Gly Met Gly Cys Ser 210 215 220	672
gcc ggc gtt ata gcc att gat cta gca aag gac ttg ttg cat gtc cat Ala Gly Val Ile Ala Ile Asp Leu Ala Lys Asp Leu Leu His Val His 225 230 235 240	720
aaa aat acg tat gct ctt gtg gtg agc aca gag aac atc act tat aac Lys Asn Thr Tyr Ala Leu Val Val Ser Thr Glu Asn Ile Thr Tyr Asn 245 250 255	768
att tac gct ggt gat aat agg tcc atg atg gtt tca aat tgc ttg ttc Ile Tyr Ala Gly Asp Asn Arg Ser Met Met Val Ser Asn Cys Leu Phe 260 265 270	816
cgt gtt ggt ggg gcc gct att ttg ctc tcc aac aag cct gga gat cgt Arg Val Gly Gly Ala Ala Ile Leu Leu Ser Asn Lys Pro Gly Asp Arg 275 280 285	864
aga cgg tcc aag tac gag cta gtt cac acg gtt cga acg cat acc gga Arg Arg Ser Lys Tyr Glu Leu Val His Thr Val Arg Thr His Thr Gly 290 295 300	912
gct gac ggc aag tct ttt cgt tgc gtg caa caa gga gac gat gag aac Ala Asp Gly Lys Ser Phe Arg Cys Val Gln Gln Gly Asp Asp Glu Asn 305 310 315 320	960
ggc aaa atc gga gtg agt ttg tcc aag gac ata acc gat gtt gct ggt Gly Lys Ile Gly Val Ser Leu Ser Lys Asp Ile Thr Asp Val Ala Gly 325 330 335	1008
cga acg gtt aag aaa aac ata gca acg ttg ggt ccg ttg att ctt ccg	1056

Arg	Thr	Val	Lys	Lys	Asn	Ile	Ala	Thr	Leu	Gly	Pro	Leu	Ile	Leu	Pro		
			340					345					350				
tta	agc	gag	aaa	ctt	ctt	ttt	ttc	gtt	acc	ttc	atg	ggc	aag	aaa	ctt	1104	
Leu	Ser	Glu	Lys	Leu	Leu	Phe	Phe	Val	Thr	Phe	Met	Gly	Lys	Lys	Leu		
		355					360					365					
ttc	aaa	gat	aaa	atc	aaa	cat	tac	tac	gtc	ccg	gat	ttc	aaa	ctt	gct	1152	
Phe	Lys	Asp	Lys	Ile	Lys	His	Tyr	Tyr	Val	Pro	Asp	Phe	Lys	Leu	Ala		
		370				375					380						
att	gac	cat	ttt	tgt	ata	cat	gcc	gga	ggc	aga	gcc	gtg	att	gat	gtg	1200	
Ile	Asp	His	Phe	Cys	Ile	His	Ala	Gly	Gly	Arg	Ala	Val	Ile	Asp	Val		
	385				390					395					400		
cta	gag	aag	aac	cta	gcc	cta	gca	ccg	atc	gat	gta	gag	gca	tca	aga	1248	
Leu	Glu	Lys	Asn	Leu	Ala	Leu	Ala	Pro	Ile	Asp	Val	Glu	Ala	Ser	Arg		
			405					410						415			
tca	acg	tta	cat	aga	ttt	gga	aac	act	tca	tct	agc	tca	ata	tgg	tat	1296	
Ser	Thr	Leu	His	Arg	Phe	Gly	Asn	Thr	Ser	Ser	Ser	Ser	Ile	Trp	Tyr		
			420					425					430				
gag	ttg	gca	tac	ata	gaa	gca	aaa	gga	agg	atg	aag	aaa	ggg	aat	aaa	1344	
Glu	Leu	Ala	Tyr	Ile	Glu	Ala	Lys	Gly	Arg	Met	Lys	Lys	Gly	Asn	Lys		
		435				440						445					
gtt	tgg	cag	att	gct	tta	ggg	tca	ggc	ttt	aag	tgt	aac	agt	gca	gtt	1392	
Val	Trp	Gln	Ile	Ala	Leu	Gly	Ser	Gly	Phe	Lys	Cys	Asn	Ser	Ala	Val		
	450					455					460						
tgg	gtg	gct	cta	aac	aat	gtc	aaa	gct	tcg	aca	aat	agt	cct	tgg	gaa	1440	
Trp	Val	Ala	Leu	Asn	Asn	Val	Lys	Ala	Ser	Thr	Asn	Ser	Pro	Trp	Glu		
	465				470				475						480		
cac	tgc	atc	gac	aga	tac	ccg	gtc	aaa	att	gat	tct	gat	tca	ggg	aag	1488	
His	Cys	Ile	Asp	Arg	Tyr	Pro	Val	Lys	Ile	Asp	Ser	Asp	Ser	Gly	Lys		
			485					490						495			
tca	gag	act	cgt	gtc	cca	aac	ggg	cgg	tcc	taa						1521	
Ser	Glu	Thr	Arg	Val	Pro	Asn	Gly	Arg	Ser								
		500					505										

<210> 12

<211> 506

<212> PRT

<213> Artificial Sequence

<220>

<223> 5' 114 amino acids from *A. thaliana* FAE1 (SEQ ID NO:2) and 3' 392 amino acids from *B. napus* elongase KCS (SEQ ID NO:4) having mutations at residues 91 and 92; designated At114 L91C K92R

<400> 12

Met Thr Ser Val Asn Val Lys Leu Leu Tyr Arg Tyr Val Leu Thr Asn

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Phe	Phe	Asn	Leu	Cys	Leu	Phe	Pro	Leu	Thr	Ala	Phe	Leu	Ala	Gly Lys
			20					25				30		
Ala	Ser	Arg	Leu	Thr	Ile	Asn	Asp	Leu	His	Asn	Phe	Leu	Ser	Tyr Leu
		35					40					45		
Gln	His	Asn	Leu	Ile	Thr	Val	Thr	Leu	Leu	Phe	Ala	Phe	Thr	Val Phe
	50					55				60				
Gly	Leu	Val	Leu	Tyr	Ile	Val	Thr	Arg	Pro	Asn	Pro	Val	Tyr	Leu Val
65					70					75				80
Asp	Tyr	Ser	Cys	Tyr	Leu	Pro	Pro	Pro	His	Cys	Arg	Val	Ser	Val Ser
			85						90				95	
Lys	Val	Met	Asp	Ile	Phe	Tyr	Gln	Ile	Arg	Lys	Ala	Asp	Thr	Ser Ser
			100					105				110		
Arg	Asn	Gly	Thr	Cys	Asp	Asn	Ser	Ser	Trp	Leu	Asp	Phe	Leu	Arg Lys
		115					120				125			
Ile	Gln	Glu	Arg	Ser	Gly	Leu	Gly	Asp	Glu	Thr	His	Gly	Pro	Glu Gly
	130				135					140				
Leu	Leu	Gln	Val	Pro	Pro	Arg	Lys	Thr	Phe	Ala	Ala	Ala	Arg	Glu Glu
145					150				155					160
Thr	Glu	Gln	Val	Ile	Ile	Gly	Ala	Leu	Glu	Asn	Leu	Phe	Lys	Asn Thr
			165					170					175	
Asn	Val	Asn	Pro	Lys	Asp	Ile	Gly	Ile	Leu	Val	Val	Asn	Ser	Ser Met
			180				185					190		
Phe	Asn	Pro	Thr	Pro	Ser	Leu	Ser	Ala	Met	Val	Val	Asn	Thr	Phe Lys
		195					200				205			
Leu	Arg	Ser	Asn	Val	Arg	Ser	Phe	Asn	Leu	Gly	Gly	Met	Gly	Cys Ser
	210				215					220				
Ala	Gly	Val	Ile	Ala	Ile	Asp	Leu	Ala	Lys	Asp	Leu	Leu	His	Val His
225					230				235					240
Lys	Asn	Thr	Tyr	Ala	Leu	Val	Val	Ser	Thr	Glu	Asn	Ile	Thr	Tyr Asn
			245					250					255	
Ile	Tyr	Ala	Gly	Asp	Asn	Arg	Ser	Met	Met	Val	Ser	Asn	Cys	Leu Phe
		260					265					270		
Arg	Val	Gly	Gly	Ala	Ala	Ile	Leu	Ser	Asn	Lys	Pro	Gly	Asp	Arg
		275				280				285				
Arg	Arg	Ser	Lys	Tyr	Glu	Leu	Val	His	Thr	Val	Arg	Thr	His	Thr Gly
	290				295				300					
Ala	Asp	Gly	Lys	Ser	Phe	Arg	Cys	Val	Gln	Gln	Gly	Asp	Asp	Glu Asn
305					310				315					320
Gly	Lys	Ile	Gly	Val	Ser	Leu	Ser	Lys	Asp	Ile	Thr	Asp	Val	Ala Gly
			325					330					335	
Arg	Thr	Val	Lys	Lys	Asn	Ile	Ala	Thr	Leu	Gly	Pro	Leu	Ile	Leu Pro
		340					345					350		
Leu	Ser	Glu	Lys	Leu	Leu	Phe	Phe	Val	Thr	Phe	Met	Gly	Lys	Lys Leu
		355				360				365				
Phe	Lys	Asp	Lys	Ile	Lys	His	Tyr	Tyr	Val	Pro	Asp	Phe	Lys	Leu Ala
	370				375					380				
Ile	Asp	His	Phe	Cys	Ile	His	Ala	Gly	Gly	Arg	Ala	Val	Ile	Asp Val
385				390				395						400
Leu	Glu	Lys	Asn	Leu	Ala	Leu	Ala	Pro	Ile	Asp	Val	Glu	Ala	Ser Arg
			405					410					415	
Ser	Thr	Leu	His	Arg	Phe	Gly	Asn	Thr	Ser	Ser	Ser	Ser	Ile	Trp Tyr
		420					425					430		
Glu	Leu	Ala	Tyr	Ile	Glu	Ala	Lys	Gly	Arg	Met	Lys	Lys	Gly	Asn Lys
	435				440					445				
Val	Trp	Gln	Ile	Ala	Leu	Gly	Ser	Gly	Phe	Lys	Cys	Asn	Ser	Ala Val
450					455					460				

Trp Val Ala Leu Asn Asn Val Lys Ala Ser Thr Asn Ser Pro Trp Glu
 465 470 475 480
 His Cys Ile Asp Arg Tyr Pro Val Lys Ile Asp Ser Asp Ser Gly Lys
 485 490 495
 Ser Glu Thr Arg Val Pro Asn Gly Arg Ser
 500 505

<210> 13

<211> 1521

<212> DNA

<213> Artificial Sequence

<220>

<223> 5' 342 bp from A. thaliana FAE1 (SEQ ID NO:1) and
 3' 1179 bp from B. napus elongase KCS (SEQ ID
 NO:3), having a mutation at position 275;
 designated At114 K92R

<221> CDS

<222> (1)...(1518)

<400> 13

atg acg tcc gtt aac gtt aag ctc ctt tac cgt tat gtc tta acc aac 48
 Met Thr Ser Val Asn Val Lys Leu Leu Tyr Arg Tyr Val Leu Thr Asn
 1 5 10 15

ttt ttc aac ctc tgt ttg ttc ccg tta acg gcg ttc ctc gcc gga aaa 96
 Phe Phe Asn Leu Cys Leu Phe Pro Leu Thr Ala Phe Leu Ala Gly Lys
 20 25 30

gcc tct cgg ctt acc ata aac gat ctc cac aac ttc ctt tcc tat ctc 144
 Ala Ser Arg Leu Thr Ile Asn Asp Leu His Asn Phe Leu Ser Tyr Leu
 35 40 45

caa cac aac ctt ata aca gta act tta ctc ttt gct ttc act gtt ttc 192
 Gln His Asn Leu Ile Thr Val Thr Leu Leu Phe Ala Phe Thr Val Phe
 50 55 60

ggg ttg gtt ctc tac atc gta acc cga ccc aat ccg gtt tat ctc gtt 240
 Gly Leu Val Leu Tyr Ile Val Thr Arg Pro Asn Pro Val Tyr Leu Val
 65 70 75 80

gac tac tcg tgt tac ctt ccg cca ccg cat ctc aga gtt agt gtc tct 288
 Asp Tyr Ser Cys Tyr Leu Pro Pro Pro His Leu Arg Val Ser Val Ser
 85 90 95

aaa gtc atg gat att ttc tac caa ata aga aaa gct gat act tct tca 336
 Lys Val Met Asp Ile Phe Tyr Gln Ile Arg Lys Ala Asp Thr Ser Ser
 100 105 110

ccg aac ggc acg tgt gat gat tcg tcg tgg ctt gac ttc ttg agg aag 384
 Arg Asn Gly Thr Cys Asp Asp Ser Ser Trp Leu Asp Phe Leu Arg Lys
 115 120 125

att caa gaa cgt tca ggt cta ggc gat gaa act cac ggg ccc gag ggg 432
 Ile Gln Glu Arg Ser Gly Leu Gly Asp Glu Thr His Gly Pro Glu Gly
 130 135 140

ctg ctt cag gtc cct ccc cgg aag act ttt gcg gcg gcg cgt gaa gag	480
Leu Leu Gln Val Pro Pro Arg Lys Thr Phe Ala Ala Ala Arg Glu Glu	
145 150 155 160	
acg gag caa gtt atc att ggt gcg cta gaa aat cta ttc aag aac acc	528
Thr Glu Gln Val Ile Ile Gly Ala Leu Glu Asn Leu Phe Lys Asn Thr	
165 170 175	
aac gtt aac cct aaa gat ata ggt ata ctt gtg gtg aac tca agc atg	576
Asn Val Asn Pro Lys Asp Ile Gly Ile Leu Val Val Asn Ser Ser Met	
180 185 190	
ttt aat cca act cca tcg ctc tcc gcg atg gtc gtt aac act ttc aag	624
Phe Asn Pro Thr Pro Ser Leu Ser Ala Met Val Val Asn Thr Phe Lys	
195 200 205	
ctc cga agc aac gta aga agc ttt aac ctt ggt ggc atg ggt tgt agt	672
Leu Arg Ser Asn Val Arg Ser Phe Asn Leu Gly Gly Met Gly Cys Ser	
210 215 220	
gcc ggc gtt ata gcc att gat cta gca aag gac ttg ttg cat gtc cat	720
Ala Gly Val Ile Ala Ile Asp Leu Ala Lys Asp Leu Leu His Val His	
225 230 235 240	
aaa aat acg tat gct ctt gtg gtg agc aca gag aac atc act tat aac	768
Lys Asn Thr Tyr Ala Leu Val Val Ser Thr Glu Asn Ile Thr Tyr Asn	
245 250 255	
att tac gct ggt gat aat agg tcc atg atg gtt tca aat tgc ttg ttc	816
Ile Tyr Ala Gly Asp Asn Arg Ser Met Met Val Ser Asn Cys Leu Phe	
260 265 270	
cgt gtt ggt ggg gcc gct att ttg ctc tcc aac aag cct gga gat cgt	864
Arg Val Gly Gly Ala Ala Ile Leu Leu Ser Asn Lys Pro Gly Asp Arg	
275 280 285	
aga cgg tcc aag tac gag cta gtt cac acg gtt cga acg cat acc gga	912
Arg Arg Ser Lys Tyr Glu Leu Val His Thr Val Arg Thr His Thr Gly	
290 295 300	
gct gac ggc aag tct ttt cgt tgc gtg caa caa gga gac gat gag aac	960
Ala Asp Gly Lys Ser Phe Arg Cys Val Gln Gln Gly Asp Asp Glu Asn	
305 310 315 320	
ggc aaa atc gga gtg agt ttg tcc aag gac ata acc gat gtt gct ggt	1008
Gly Lys Ile Gly Val Ser Leu Ser Lys Asp Ile Thr Asp Val Ala Gly	
325 330 335	
cga acg gtt aag aaa aac ata gca acg ttg ggt ccg ttg att ctt ccg	1056
Arg Thr Val Lys Lys Asn Ile Ala Thr Leu Gly Pro Leu Ile Leu Pro	
340 345 350	
tta agc gag aaa ctt ctt ttt ttc gtt acc ttc atg ggc aag aaa ctt	1104
Leu Ser Glu Lys Leu Leu Phe Phe Val Thr Phe Met Gly Lys Lys Leu	
355 360 365	

ttc aaa gat aaa atc aaa cat tac tac gtc ccg gat ttc aaa ctt gct 1152
 Phe Lys Asp Lys Ile Lys His Tyr Tyr Val Pro Asp Phe Lys Leu Ala
 370 375 380

att gac cat ttt tgt ata cat gcc gga ggc aga gcc gtg att gat gtg 1200
 Ile Asp His Phe Cys Ile His Ala Gly Gly Arg Ala Val Ile Asp Val
 385 390 395 400

cta gag aag aac cta gcc cta gca ccg atc gat gta gag gca tca aga 1248
 Leu Glu Lys Asn Leu Ala Leu Ala Pro Ile Asp Val Glu Ala Ser Arg
 405 410 415

tca acg tta cat aga ttt gga aac act tca tct agc tca ata tgg tat 1296
 Ser Thr Leu His Arg Phe Gly Asn Thr Ser Ser Ser Ser Ile Trp Tyr
 420 425 430

gag ttg gca tac ata gaa gca aaa gga agg atg aag aaa ggt aat aaa 1344
 Glu Leu Ala Tyr Ile Glu Ala Lys Gly Arg Met Lys Lys Gly Asn Lys
 435 440 445

gtt tgg cag att gct tta ggg tca ggc ttt aag tgt aac agt gca gtt 1392
 Val Trp Gln Ile Ala Leu Gly Ser Gly Phe Lys Cys Asn Ser Ala Val
 450 455 460

tgg gtg gct cta aac aat gtc aaa gct tcg aca aat agt cct tgg gaa 1440
 Trp Val Ala Leu Asn Asn Val Lys Ala Ser Thr Asn Ser Pro Trp Glu
 465 470 475 480

cac tgc atc gac aga tac ccg gtc aaa att gat tct gat tca ggt aag 1488
 His Cys Ile Asp Arg Tyr Pro Val Lys Ile Asp Ser Asp Ser Gly Lys
 485 490 495

tca gag act cgt gtc cca aac ggt cgg tcc taa 1521
 Ser Glu Thr Arg Val Pro Asn Gly Arg Ser
 500 505

<210> 14

<211> 506

<212> PRT

<213> Artificial Sequence

<220>

<223> 5' 114 amino acids from *A. thaliana* FAEL (SEQ ID NO:2) and 3' 392 amino acids from *B. napus* elongase KCS (SEQ ID NO:4), having a mutation at position 92; designated At114 K92R

<400> 14

Met	Thr	Ser	Val	Asn	Val	Lys	Leu	Leu	Tyr	Arg	Tyr	Val	Leu	Thr	Asn
1				5					10					15	
Phe	Phe	Asn	Leu	Cys	Leu	Phe	Pro	Leu	Thr	Ala	Phe	Leu	Ala	Gly	Lys
			20					25					30		
Ala	Ser	Arg	Leu	Thr	Ile	Asn	Asp	Leu	His	Asn	Phe	Leu	Ser	Tyr	Leu
		35					40					45			
Gln	His	Asn	Leu	Ile	Thr	Val	Thr	Leu	Leu	Phe	Ala	Phe	Thr	Val	Phe
	50					55					60				

Gly Leu Val Leu Tyr Ile Val Thr Arg Pro Asn Pro Val Tyr Leu Val
 65 70 75 80
 Asp Tyr Ser Cys Tyr Leu Pro Pro Pro His Leu Arg Val Ser Val Ser
 85 90 95
 Lys Val Met Asp Ile Phe Tyr Gln Ile Arg Lys Ala Asp Thr Ser Ser
 100 105 110
 Arg Asn Gly Thr Cys Asp Asp Ser Ser Trp Leu Asp Phe Leu Arg Lys
 115 120 125
 Ile Gln Glu Arg Ser Gly Leu Gly Asp Glu Thr His Gly Pro Glu Gly
 130 135 140
 Leu Leu Gln Val Pro Pro Arg Lys Thr Phe Ala Ala Ala Arg Glu Glu
 145 150 155 160
 Thr Glu Gln Val Ile Ile Gly Ala Leu Glu Asn Leu Phe Lys Asn Thr
 165 170 175
 Asn Val Asn Pro Lys Asp Ile Gly Ile Leu Val Val Asn Ser Ser Met
 180 185 190
 Phe Asn Pro Thr Pro Ser Leu Ser Ala Met Val Val Asn Thr Phe Lys
 195 200 205
 Leu Arg Ser Asn Val Arg Ser Phe Asn Leu Gly Gly Met Gly Cys Ser
 210 215 220
 Ala Gly Val Ile Ala Ile Asp Leu Ala Lys Asp Leu Leu His Val His
 225 230 235 240
 Lys Asn Thr Tyr Ala Leu Val Val Ser Thr Glu Asn Ile Thr Tyr Asn
 245 250 255
 Ile Tyr Ala Gly Asp Asn Arg Ser Met Met Val Ser Asn Cys Leu Phe
 260 265 270
 Arg Val Gly Gly Ala Ala Ile Leu Leu Ser Asn Lys Pro Gly Asp Arg
 275 280 285
 Arg Arg Ser Lys Tyr Glu Leu Val His Thr Val Arg Thr His Thr Gly
 290 295 300
 Ala Asp Gly Lys Ser Phe Arg Cys Val Gln Gln Gly Asp Asp Glu Asn
 305 310 315 320
 Gly Lys Ile Gly Val Ser Leu Ser Lys Asp Ile Thr Asp Val Ala Gly
 325 330 335
 Arg Thr Val Lys Lys Asn Ile Ala Thr Leu Gly Pro Leu Ile Leu Pro
 340 345 350
 Leu Ser Glu Lys Leu Leu Phe Phe Val Thr Phe Met Gly Lys Lys Leu
 355 360 365
 Phe Lys Asp Lys Ile Lys His Tyr Tyr Val Pro Asp Phe Lys Leu Ala
 370 375 380
 Ile Asp His Phe Cys Ile His Ala Gly Gly Arg Ala Val Ile Asp Val
 385 390 395 400
 Leu Glu Lys Asn Leu Ala Leu Ala Pro Ile Asp Val Glu Ala Ser Arg
 405 410 415
 Ser Thr Leu His Arg Phe Gly Asn Thr Ser Ser Ser Ser Ile Trp Tyr
 420 425 430
 Glu Leu Ala Tyr Ile Glu Ala Lys Gly Arg Met Lys Lys Gly Asn Lys
 435 440 445
 Val Trp Gln Ile Ala Leu Gly Ser Gly Phe Lys Cys Asn Ser Ala Val
 450 455 460
 Trp Val Ala Leu Asn Asn Val Lys Ala Ser Thr Asn Ser Pro Trp Glu
 465 470 475 480
 His Cys Ile Asp Arg Tyr Pro Val Lys Ile Asp Ser Asp Ser Gly Lys
 485 490 495
 Ser Glu Thr Arg Val Pro Asn Gly Arg Ser
 500 505

<210> 15
 <211> 1521
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> 5' 342 bp from A. thaliana FAE1 (SEQ ID NO:1) and
 3' 1179 bp from B. napus elongase KCS (SEQ ID
 NO:3), having a mutation at position 920;
 designated At114 G307D; hypothetical

<221> CDS
 <222> (1)...(1518)

<400> 15
 atg acg tcc gtt aac gtt aag ctc ctt tac cgt tat gtc tta acc aac 48
 Met Thr Ser Val Asn Val Lys Leu Leu Tyr Arg Tyr Val Leu Thr Asn
 1 5 10 15

ttt ttc aac ctc tgt ttg ttc ccg tta acg gcg ttc ctc gcc gga aaa 96
 Phe Phe Asn Leu Cys Leu Phe Pro Leu Thr Ala Phe Leu Ala Gly Lys
 20 25 30

gcc tct cgg ctt acc ata aac gat ctc cac aac ttc ctt tcc tat ctc 144
 Ala Ser Arg Leu Thr Ile Asn Asp Leu His Asn Phe Leu Ser Tyr Leu
 35 40 45

caa cac aac ctt ata aca gta act tta ctc ttt gct ttc act gtt ttc 192
 Gln His Asn Leu Ile Thr Val Thr Leu Leu Phe Ala Phe Thr Val Phe
 50 55 60

ggg ttg gtt ctc tac atc gta acc cga ccc aat ccg gtt tat ctc gtt 240
 Gly Leu Val Leu Tyr Ile Val Thr Arg Pro Asn Pro Val Tyr Leu Val
 65 70 75 80

gac tac tcg tgt tac ctt ccg cca ccg cat ctc aaa gtt agt gtc tct 288
 Asp Tyr Ser Cys Tyr Leu Pro Pro His Leu Lys Val Ser Val Ser
 85 90 95

aaa gtc atg gat att ttc tac caa ata aga aaa gct gat act tct tca 336
 Lys Val Met Asp Ile Phe Tyr Gln Ile Arg Lys Ala Asp Thr Ser Ser
 100 105 110

cgg aac ggc acg tgt gat gat tcg tcg tgg ctt gac ttc ttg agg aag 384
 Arg Asn Gly Thr Cys Asp Asp Ser Ser Trp Leu Asp Phe Leu Arg Lys
 115 120 125

att caa gaa cgt tca ggt cta ggc gat gaa act cac ggg ccc gag ggg 432
 Ile Gln Glu Arg Ser Gly Leu Gly Asp Glu Thr His Gly Pro Glu Gly
 130 135 140

ctg ctt cag gtc cct ccc ccg aag act ttt gcg gcg gcg cgt gaa gag 480
 Leu Leu Gln Val Pro Pro Arg Lys Thr Phe Ala Ala Ala Arg Glu Glu
 145 150 155 160

acg gag caa gtt atc att ggt gcg cta gaa aat cta ttc aag aac acc 528
 Thr Glu Gln Val Ile Ile Gly Ala Leu Glu Asn Leu Phe Lys Asn Thr

	165	170	175	
	aac gtt aac cct aaa gat ata ggt ata ctt gtg gtg aac tca agc atg			576
	Asn Val Asn Pro Lys Asp Ile Gly Ile Leu Val Val Asn Ser Ser Met			
	180	185	190	
	ttt aat cca act cca tcg ctc tcc gcg atg gtc gtt aac act ttc aag			624
	Phe Asn Pro Thr Pro Ser Leu Ser Ala Met Val Val Asn Thr Phe Lys			
	195	200	205	
	ctc cga agc aac gta aga agc ttt aac ctt ggt ggc atg ggt tgt agt			672
	Leu Arg Ser Asn Val Arg Ser Phe Asn Leu Gly Gly Met Gly Cys Ser			
	210	215	220	
	gcc ggc gtt ata gcc att gat cta gca aag gac ttg ttg cat gtc cat			720
	Ala Gly Val Ile Ala Ile Asp Leu Ala Lys Asp Leu Leu His Val His			
	225	230	235	240
	aaa aat acg tat gct ctt gtg gtg agc aca gag aac atc act tat aac			768
	Lys Asn Thr Tyr Ala Leu Val Val Ser Thr Glu Asn Ile Thr Tyr Asn			
	245	250	255	
	att tac gct ggt gat aat agg tcc atg atg gtt tca aat tgc ttg ttc			816
	Ile Tyr Ala Gly Asp Asn Arg Ser Met Met Val Ser Asn Cys Leu Phe			
	260	265	270	
	cgt gtt ggt ggg gcc gct att ttg ctc tcc aac aag cct gga gat cgt			864
	Arg Val Gly Gly Ala Ala Ile Leu Leu Ser Asn Lys Pro Gly Asp Arg			
	275	280	285	
	aga cgg tcc aag tac gag cta gtt cac acg gtt cga acg cat acc gga			912
	Arg Arg Ser Lys Tyr Glu Leu Val His Thr Val Arg Thr His Thr Gly			
	290	295	300	
	gct gac gac aag tct ttt cgt tgc gtg caa caa gga gac gat gag aac			960
	Ala Asp Asp Lys Ser Phe Arg Cys Val Gln Gln Gly Asp Asp Glu Asn			
	305	310	315	320
	ggc aaa atc gga gtg agt ttg tcc aag gac ata acc gat gtt gct ggt			1008
	Gly Lys Ile Gly Val Ser Leu Ser Lys Asp Ile Thr Asp Val Ala Gly			
	325	330	335	
	cga acg gtt aag aaa aac ata gca acg ttg ggt ccg ttg att ctt ccg			1056
	Arg Thr Val Lys Lys Asn Ile Ala Thr Leu Gly Pro Leu Ile Leu Pro			
	340	345	350	
	tta agc gag aaa ctt ctt ttt ttc gtt acc ttc atg ggc aag aaa ctt			1104
	Leu Ser Glu Lys Leu Leu Phe Phe Val Thr Phe Met Gly Lys Lys Leu			
	355	360	365	
	ttc aaa gat aaa atc aaa cat tac tac gtc ccg gat ttc aaa ctt gct			1152
	Phe Lys Asp Lys Ile Lys His Tyr Tyr Val Pro Asp Phe Lys Leu Ala			
	370	375	380	
	att gac cat ttt tgt ata cat gcc gga ggc aga gcc gtg att gat gtg			1200
	Ile Asp His Phe Cys Ile His Ala Gly Gly Arg Ala Val Ile Asp Val			
	385	390	395	400

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cta gag aag aac cta gcc cta gca ccg atc gat gta gag gca tca aga 1248
 Leu Glu Lys Asn Leu Ala Leu Ala Pro Ile Asp Val Glu Ala Ser Arg
 405 410 415

tca acg tta cat aga ttt gga aac act tca tct agc tca ata tgg tat 1296
 Ser Thr Leu His Arg Phe Gly Asn Thr Ser Ser Ser Ile Trp Tyr
 420 425 430

gag ttg gca tac ata gaa gca aaa gga agg atg aag aaa ggt aat aaa 1344
 Glu Leu Ala Tyr Ile Glu Ala Lys Gly Arg Met Lys Lys Gly Asn Lys
 435 440 445

gtt tgg cag att gct tta ggg tca ggc ttt aag tgt aac agt gca gtt 1392
 Val Trp Gln Ile Ala Leu Gly Ser Gly Phe Lys Cys Asn Ser Ala Val
 450 455 460

tgg gtg gct cta aac aat gtc aaa gct tgc aca aat agt cct tgg gaa 1440
 Trp Val Ala Leu Asn Asn Val Lys Ala Ser Thr Asn Ser Pro Trp Glu
 465 470 475 480

cac tgc atc gac aga tac ccg gtc aaa att gat tct gat tca ggt aag 1488
 His Cys Ile Asp Arg Tyr Pro Val Lys Ile Asp Ser Asp Ser Gly Lys
 485 490 495

tca gag act cgt gtc caa aac ggt cgg tcc taa 1521
 Ser Glu Thr Arg Val Gln Asn Gly Arg Ser
 500 505

<210> 16

<211> 506

<212> PRT

<213> Artificial Sequence

<220>

<223> 5' 114 amino acids from A. thaliana FAE1 (SEQ ID
 NO:2) and 3' 392 amino acids from B. napus
 elongase KCS (SEQ ID NO:4) having mutation at
 residue 307; designated At114 G307D; hypothetical

<400> 16

Met Thr Ser Val Asn Val Lys Leu Leu Tyr Arg Tyr Val Leu Thr Asn
 1 5 10 15
 Phe Phe Asn Leu Cys Leu Phe Pro Leu Thr Ala Phe Leu Ala Gly Lys
 20 25 30
 Ala Ser Arg Leu Thr Ile Asn Asp Leu His Asn Phe Leu Ser Tyr Leu
 35 40 45
 Gln His Asn Leu Ile Thr Val Thr Leu Leu Phe Ala Phe Thr Val Phe
 50 55 60
 Gly Leu Val Leu Tyr Ile Val Thr Arg Pro Asn Pro Val Tyr Leu Val
 65 70 75 80
 Asp Tyr Ser Cys Tyr Leu Pro Pro Pro His Leu Lys Val Ser Val Ser
 85 90 95
 Lys Val Met Asp Ile Phe Tyr Gln Ile Arg Lys Ala Asp Thr Ser Ser
 100 105 110
 Arg Asn Gly Thr Cys Asp Asp Ser Ser Trp Leu Asp Phe Leu Arg Lys

	115		120		125										
Ile	Gln	Glu	Arg	Ser	Gly	Leu	Gly	Asp	Glu	Thr	His	Gly	Pro	Glu	Gly
	130					135					140				
Leu	Leu	Gln	Val	Pro	Pro	Arg	Lys	Thr	Phe	Ala	Ala	Ala	Arg	Glu	Glu
145						150					155				160
Thr	Glu	Gln	Val	Ile	Ile	Gly	Ala	Leu	Glu	Asn	Leu	Phe	Lys	Asn	Thr
				165						170				175	
Asn	Val	Asn	Pro	Lys	Asp	Ile	Gly	Ile	Leu	Val	Val	Asn	Ser	Ser	Met
			180					185					190		
Phe	Asn	Pro	Thr	Pro	Ser	Leu	Ser	Ala	Met	Val	Val	Asn	Thr	Phe	Lys
	195					200					205				
Leu	Arg	Ser	Asn	Val	Arg	Ser	Phe	Asn	Leu	Gly	Gly	Met	Gly	Cys	Ser
210						215					220				
Ala	Gly	Val	Ile	Ala	Ile	Asp	Leu	Ala	Lys	Asp	Leu	Leu	His	Val	His
225					230					235					240
Lys	Asn	Thr	Tyr	Ala	Leu	Val	Val	Ser	Thr	Glu	Asn	Ile	Thr	Tyr	Asn
			245						250					255	
Ile	Tyr	Ala	Gly	Asp	Asn	Arg	Ser	Met	Met	Val	Ser	Asn	Cys	Leu	Phe
	260							265					270		
Arg	Val	Gly	Gly	Ala	Ala	Ile	Leu	Leu	Ser	Asn	Lys	Pro	Gly	Asp	Arg
	275						280					285			
Arg	Arg	Ser	Lys	Tyr	Glu	Leu	Val	His	Thr	Val	Arg	Thr	His	Thr	Gly
290						295					300				
Ala	Asp	Asp	Lys	Ser	Phe	Arg	Cys	Val	Gln	Gln	Gly	Asp	Asp	Glu	Asn
305					310					315					320
Gly	Lys	Ile	Gly	Val	Ser	Leu	Ser	Lys	Asp	Ile	Thr	Asp	Val	Ala	Gly
			325						330					335	
Arg	Thr	Val	Lys	Lys	Asn	Ile	Ala	Thr	Leu	Gly	Pro	Leu	Ile	Leu	Pro
	340							345				350			
Leu	Ser	Glu	Lys	Leu	Leu	Phe	Phe	Val	Thr	Phe	Met	Gly	Lys	Lys	Leu
	355					360					365				
Phe	Lys	Asp	Lys	Ile	Lys	His	Tyr	Tyr	Val	Pro	Asp	Phe	Lys	Leu	Ala
370					375						380				
Ile	Asp	His	Phe	Cys	Ile	His	Ala	Gly	Gly	Arg	Ala	Val	Ile	Asp	Val
385					390				395						400
Leu	Glu	Lys	Asn	Leu	Ala	Leu	Ala	Pro	Ile	Asp	Val	Glu	Ala	Ser	Arg
			405					410						415	
Ser	Thr	Leu	His	Arg	Phe	Gly	Asn	Thr	Ser	Ser	Ser	Ser	Ser	Ile	Trp
	420						425					430			
Glu	Leu	Ala	Tyr	Ile	Glu	Ala	Lys	Gly	Arg	Met	Lys	Lys	Gly	Asn	Lys
	435						440					445			
Val	Trp	Gln	Ile	Ala	Leu	Gly	Ser	Gly	Phe	Lys	Cys	Asn	Ser	Ala	Val
450						455					460				
Trp	Val	Ala	Leu	Asn	Asn	Val	Lys	Ala	Ser	Thr	Asn	Ser	Pro	Trp	Glu
465				470					475						480
His	Cys	Ile	Asp	Arg	Tyr	Pro	Val	Lys	Ile	Asp	Ser	Asp	Ser	Gly	Lys
			485					490						495	
Ser	Glu	Thr	Arg	Val	Gln	Asn	Gly	Arg	Ser						
	500						505								

<210> 17

<211> 1518

<212> DNA

<213> Artificial Sequence

<220>

<223> 5' 222 bp from A. thaliana FAE1 (SEQ ID NO:1) and

3' 1296 bp from B. napus elongase KCS (SEQ ID NO:3) having a mutation at position 917; designated At74 G306D; hypothetical

<221> CDS

<222> (1)...(1515)

<400> 17

atg	acg	tcc	ggt	aac	ggt	aag	ctc	ctt	tac	cgt	tac	gtc	tta	acc	aac	48
Met	Thr	Ser	Val	Asn	Val	Lys	Leu	Leu	Tyr	Arg	Tyr	Val	Leu	Thr	Asn	
1				5					10					15		

ttt	ttc	aac	ctc	tgt	ttg	ttc	ccg	tta	acg	gcg	ttc	ctc	gcc	gga	aaa	96
Phe	Phe	Asn	Leu	Cys	Leu	Phe	Pro	Leu	Thr	Ala	Phe	Leu	Ala	Gly	Lys	
		20						25					30			

gcc	tct	cgg	ctt	acc	ata	aac	gat	ctc	cac	aac	ttc	ctt	tcc	tat	ctc	144
Ala	Ser	Arg	Leu	Thr	Ile	Asn	Asp	Leu	His	Asn	Phe	Leu	Ser	Tyr	Leu	
		35					40						45			

caa	cac	aac	ctt	ata	aca	gta	act	tta	ctc	ttt	gct	ttc	act	ggt	ttc	192
Gln	His	Asn	Leu	Ile	Thr	Val	Thr	Leu	Leu	Phe	Ala	Phe	Thr	Val	Phe	
		50					55					60				

ggg	ttg	ggt	ctc	tac	atc	gta	acc	cga	ccc	aaa	ccg	ggt	tac	ctc	ggt	240
Gly	Leu	Val	Leu	Tyr	Ile	Val	Thr	Arg	Pro	Lys	Pro	Val	Tyr	Leu	Val	
65					70					75					80	

gag	tac	tca	tgc	tac	ctt	cca	cca	acg	cat	tgt	aga	tca	agt	atc	tcc	288
Glu	Tyr	Ser	Cys	Tyr	Leu	Pro	Pro	Thr	His	Cys	Arg	Ser	Ser	Ile	Ser	
			85						90					95		

aag	gtc	atg	gat	atc	ttt	tat	caa	gta	aga	aaa	gct	gat	cct	tct	cgg	336
Lys	Val	Met	Asp	Ile	Phe	Tyr	Gln	Val	Arg	Lys	Ala	Asp	Pro	Ser	Arg	
			100					105					110			

aac	ggc	acg	tgc	gat	gac	tgc	tgc	tgg	ctt	gac	ttc	ttg	agg	aag	att	384
Asn	Gly	Thr	Cys	Asp	Asp	Ser	Ser	Trp	Leu	Asp	Phe	Leu	Arg	Lys	Ile	
		115					120					125				

caa	gaa	cgt	tca	ggg	cta	ggc	gat	gaa	act	cac	ggg	ccc	gag	ggg	ctg	432
Gln	Glu	Arg	Ser	Gly	Leu	Gly	Asp	Glu	Thr	His	Gly	Pro	Glu	Gly	Leu	
		130				135					140					

ctt	cag	gtc	cct	ccc	cgg	aag	act	ttt	gcg	gcg	gcg	cgt	gaa	gag	acg	480
Leu	Gln	Val	Pro	Pro	Arg	Lys	Thr	Phe	Ala	Ala	Ala	Arg	Glu	Glu	Thr	
145					150				155						160	

gag	caa	ggt	atc	att	ggg	gag	cta	gaa	aat	cta	ttc	aag	aac	acc	aac	528
Glu	Gln	Val	Ile	Ile	Gly	Ala	Leu	Glu	Asn	Leu	Phe	Lys	Asn	Thr	Asn	
			165					170						175		

gtt	aac	cct	aaa	gat	ata	ggg	ata	ctt	gtg	gtg	aac	tca	agc	atg	ttt	576
Val	Asn	Pro	Lys	Asp	Ile	Gly	Ile	Leu	Val	Val	Asn	Ser	Ser	Met	Phe	
			180					185					190			

aat	cca	act	cca	tgc	ctc	tcc	gag	atg	gtc	ggt	aac	act	ttc	aag	ctc	624
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Asn	Pro	Thr	Pro	Ser	Leu	Ser	Ala	Met	Val	Val	Asn	Thr	Phe	Lys	Leu	
		195					200					205				
cga	agc	aac	gta	aga	agc	ttt	aac	ctt	ggg	ggc	atg	ggg	tgt	agt	gcc	672
Arg	Ser	Asn	Val	Arg	Ser	Phe	Asn	Leu	Gly	Gly	Met	Gly	Cys	Ser	Ala	
		210				215					220					
ggc	gtt	ata	gcc	att	gat	cta	gca	aag	gac	ttg	ttg	cat	gtc	cat	aaa	720
Gly	Val	Ile	Ala	Ile	Asp	Leu	Ala	Lys	Asp	Leu	Leu	His	Val	His	Lys	
		225			230					235					240	
aat	acg	tat	gct	ctt	gtg	gtg	agc	aca	gag	aac	atc	act	tat	aac	att	768
Asn	Thr	Tyr	Ala	Leu	Val	Val	Ser	Thr	Glu	Asn	Ile	Thr	Tyr	Asn	Ile	
				245					250					255		
tac	gct	ggg	gat	aat	agg	tcc	atg	atg	gtt	tca	aat	tgc	ttg	ttc	cgt	816
Tyr	Ala	Gly	Asp	Asn	Arg	Ser	Met	Met	Val	Ser	Asn	Cys	Leu	Phe	Arg	
			260					265					270			
gtt	ggg	ggg	gcc	gct	att	ttg	ctc	tcc	aac	aag	cct	gga	gat	cgt	aga	864
Val	Gly	Gly	Ala	Ala	Ile	Leu	Leu	Ser	Asn	Lys	Pro	Gly	Asp	Arg	Arg	
			275				280					285				
cgg	tcc	aag	tac	gag	cta	gtt	cac	acg	gtt	cga	acg	cat	acc	gga	gct	912
Arg	Ser	Lys	Tyr	Glu	Leu	Val	His	Thr	Val	Arg	Thr	His	Thr	Gly	Ala	
		290				295					300					
gac	gac	aag	tct	ttt	cgt	tgc	gtg	caa	caa	gga	gac	gat	gag	aac	ggc	960
Asp	Asp	Lys	Ser	Phe	Arg	Cys	Val	Gln	Gln	Gly	Asp	Asp	Glu	Asn	Gly	
		305			310					315					320	
aaa	atc	gga	gtg	agt	ttg	tcc	aag	gac	ata	acc	gat	gtt	gct	ggg	cga	1008
Lys	Ile	Gly	Val	Ser	Leu	Ser	Lys	Asp	Ile	Thr	Asp	Val	Ala	Gly	Arg	
				325					330					335		
acg	gtt	aag	aaa	aac	ata	gca	acg	ttg	ggg	ccg	ttg	att	ctt	ccg	tta	1056
Thr	Val	Lys	Lys	Asn	Ile	Ala	Thr	Leu	Gly	Pro	Leu	Ile	Leu	Pro	Leu	
			340					345					350			
agc	gag	aaa	ctt	ctt	ttt	ttc	gtt	acc	ttc	atg	ggc	aag	aaa	ctt	ttc	1104
Ser	Glu	Lys	Leu	Leu	Phe	Phe	Val	Thr	Phe	Met	Gly	Lys	Lys	Leu	Phe	
		355					360					365				
aaa	gat	aaa	atc	aaa	cat	tac	tac	gtc	ccg	gat	ttc	aaa	ctt	gct	att	1152
Lys	Asp	Lys	Ile	Lys	His	Tyr	Tyr	Val	Pro	Asp	Phe	Lys	Leu	Ala	Ile	
		370				375					380					
gac	cat	ttt	tgt	ata	cat	gcc	gga	ggc	aga	gcc	gtg	att	gat	gtg	cta	1200
Asp	His	Phe	Cys	Ile	His	Ala	Gly	Gly	Arg	Ala	Val	Ile	Asp	Val	Leu	
		385			390					395					400	
gag	aag	aac	cta	gcc	cta	gca	ccg	atc	gat	gta	gag	gca	tca	aga	tca	1248
Glu	Lys	Asn	Leu	Ala	Leu	Ala	Pro	Ile	Asp	Val	Glu	Ala	Ser	Arg	Ser	
			405					410					415			
acg	tta	cat	aga	ttt	gga	aac	act	tca	tct	agc	tca	ata	tggt	tat	gag	1296
Thr	Leu	His	Arg	Phe	Gly	Asn	Thr	Ser	Ser	Ser	Ser	Ile	Trp	Tyr	Glu	

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Abstract

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<220>
<223> 5' 74 amino acids from A. thaliana FAE1 (SEQ ID
      NO:2) and 3' 431 amino acids from B. napus
      elongase KCS (SEQ ID NO:4) having a mutation at
      residue 306; designated At74 G306D; hypothetical
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<400> 18																
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		20						25					30			
Ala	Ser	Arg	Leu	Thr	Ile	Asn	Asp	Leu	His	Asn	Phe	Leu	Ser	Tyr	Leu	
		35					40					45				
Gln	His	Asn	Leu	Ile	Thr	Val	Thr	Leu	Leu	Phe	Ala	Phe	Thr	Val	Phe	
	50					55					60					
Gly	Leu	Val	Leu	Tyr	Ile	Val	Thr	Arg	Pro	Lys	Pro	Val	Tyr	Leu	Val	
65					70					75					80	
Glu	Tyr	Ser	Cys	Tyr	Leu	Pro	Pro	Thr	His	Cys	Arg	Ser	Ser	Ile	Ser	
				85					90					95		
Lys	Val	Met	Asp	Ile	Phe	Tyr	Gln	Val	Arg	Lys	Ala	Asp	Pro	Ser	Arg	
		100						105					110			
Asn	Gly	Thr	Cys	Asp	Asp	Ser	Ser	Trp	Leu	Asp	Phe	Leu	Arg	Lys	Ile	
		115					120					125				
Gln	Glu	Arg	Ser	Gly	Leu	Gly	Asp	Glu	Thr	His	Gly	Pro	Glu	Gly	Leu	
	130					135					140					
Leu	Gln	Val	Pro	Pro	Arg	Lys	Thr	Phe	Ala	Ala	Ala	Arg	Glu	Glu	Thr	
145					150					155					160	
Glu	Gln	Val	Ile	Ile	Gly	Ala	Leu	Glu	Asn	Leu	Phe	Lys	Asn	Thr	Asn	
				165					170					175		

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Val Asn Pro Lys Asp Ile Gly Ile Leu Val Val Asn Ser Ser Met Phe
      180      185      190
Asn Pro Thr Pro Ser Leu Ser Ala Met Val Val Asn Thr Phe Lys Leu
      195      200      205
Arg Ser Asn Val Arg Ser Phe Asn Leu Gly Gly Met Gly Cys Ser Ala
      210      215      220
Gly Val Ile Ala Ile Asp Leu Ala Lys Asp Leu Leu His Val His Lys
      225      230      235      240
Asn Thr Tyr Ala Leu Val Val Ser Thr Glu Asn Ile Thr Tyr Asn Ile
      245      250      255
Tyr Ala Gly Asp Asn Arg Ser Met Met Val Ser Asn Cys Leu Phe Arg
      260      265      270
Val Gly Gly Ala Ala Ile Leu Leu Ser Asn Lys Pro Gly Asp Arg Arg
      275      280      285
Arg Ser Lys Tyr Glu Leu Val His Thr Val Arg Thr His Thr Gly Ala
      290      295      300
Asp Asp Lys Ser Phe Arg Cys Val Gln Gln Gly Asp Asp Glu Asn Gly
      305      310      315      320
Lys Ile Gly Val Ser Leu Ser Lys Asp Ile Thr Asp Val Ala Gly Arg
      325      330      335
Thr Val Lys Lys Asn Ile Ala Thr Leu Gly Pro Leu Ile Leu Pro Leu
      340      345      350
Ser Glu Lys Leu Leu Phe Phe Val Thr Phe Met Gly Lys Lys Leu Phe
      355      360      365
Lys Asp Lys Ile Lys His Tyr Tyr Val Pro Asp Phe Lys Leu Ala Ile
      370      375      380
Asp His Phe Cys Ile His Ala Gly Gly Arg Ala Val Ile Asp Val Leu
      385      390      395      400
Glu Lys Asn Leu Ala Leu Ala Pro Ile Asp Val Glu Ala Ser Arg Ser
      405      410      415
Thr Leu His Arg Phe Gly Asn Thr Ser Ser Ser Ser Ile Trp Tyr Glu
      420      425      430
Leu Ala Tyr Ile Glu Ala Lys Gly Arg Met Lys Lys Gly Asn Lys Val
      435      440      445
Trp Gln Ile Ala Leu Gly Ser Gly Phe Lys Cys Asn Ser Ala Val Trp
      450      455      460
Val Ala Leu Asn Asn Val Lys Ala Ser Thr Asn Ser Pro Trp Glu His
      465      470      475      480
Cys Ile Asp Arg Tyr Pro Val Lys Ile Asp Ser Asp Ser Gly Lys Ser
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Glu Thr Arg Val Gln Asn Gly Arg Ser
      500      505

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<210> 19

<211> 1521

<212> DNA

<213> Artificial Sequence

<220>

<223> 5' 342 bp from A. thaliana FAE1 (SEQ ID NO:1) and
3' 1179 bp from B. napus elongase KCS (SEQ ID
NO:3) having mutations at positions 271, 272, 275
and 920; designated At114 L91C K92R G307D;
hypothetical

<221> CDS

<222> (1) ... (1518)

<400> 19

atg acg tcc gtt aac gtt aag ctc ctt tac cgt tat gtc tta acc aac	48
Met Thr Ser Val Asn Val Lys Leu Leu Tyr Arg Tyr Val Leu Thr Asn	
1 5 10 15	
ttt ttc aac ctc tgt ttg ttc ccg tta acg gcg ttc ctc gcc gga aaa	96
Phe Phe Asn Leu Cys Leu Phe Pro Leu Thr Ala Phe Leu Ala Gly Lys	
20 25 30	
gcc tct cgg ctt acc ata aac gat ctc cac aac ttc ctt tcc tat ctc	144
Ala Ser Arg Leu Thr Ile Asn Asp Leu His Asn Phe Leu Ser Tyr Leu	
35 40 45	
caa cac aac ctt ata aca gta act tta ctc ttt gct ttc act gtt ttc	192
Gln His Asn Leu Ile Thr Val Thr Leu Leu Phe Ala Phe Thr Val Phe	
50 55 60	
ggg ttg gtt ctc tac atc gta acc cga ccc aat ccg gtt tat ctc gtt	240
Gly Leu Val Leu Tyr Ile Val Thr Arg Pro Asn Pro Val Tyr Leu Val	
65 70 75 80	
gac tac tcg tgt tac ctt ccg cca ccg cat tgc aga gtt agt gtc tct	288
Asp Tyr Ser Cys Tyr Leu Pro Pro Pro His Cys Arg Val Ser Val Ser	
85 90 95	
aaa gtc atg gat att ttc tac caa ata aga aaa gct gat act tct tca	336
Lys Val Met Asp Ile Phe Tyr Gln Ile Arg Lys Ala Asp Thr Ser Ser	
100 105 110	
cgg aac ggc acg tgt gat aat tcg tcg tgg ctt gac ttc ttg agg aag	384
Arg Asn Gly Thr Cys Asp Asn Ser Ser Trp Leu Asp Phe Leu Arg Lys	
115 120 125	
att caa gaa cgt tca ggt cta ggc gat gaa act cac ggg ccc gag ggg	432
Ile Gln Glu Arg Ser Gly Leu Gly Asp Glu Thr His Gly Pro Glu Gly	
130 135 140	
ctg ctt cag gtc cct ccc ccg aag act ttt gcg gcg gcg cgt gaa gag	480
Leu Leu Gln Val Pro Pro Arg Lys Thr Phe Ala Ala Ala Arg Glu Glu	
145 150 155 160	
acg gag caa gtt atc att ggt gcg cta gaa aat cta ttc aag aac acc	528
Thr Glu Gln Val Ile Ile Gly Ala Leu Glu Asn Leu Phe Lys Asn Thr	
165 170 175	
aac gtt aac cct aaa gat ata ggt ata ctt gtg gtg aac tca agc atg	576
Asn Val Asn Pro Lys Asp Ile Gly Ile Leu Val Val Asn Ser Ser Met	
180 185 190	
ttt aat cca act cca tcg ctc tcc gcg atg gtc gtt aac act ttc aag	624
Phe Asn Pro Thr Pro Ser Leu Ser Ala Met Val Val Asn Thr Phe Lys	
195 200 205	
ctc cga agc aac gta aga agc ttt aac ctt ggt ggc atg ggt tgt agt	672
Leu Arg Ser Asn Val Arg Ser Phe Asn Leu Gly Gly Met Gly Cys Ser	
210 215 220	

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gcc ggc gtt ata gcc att gat cta gca aag gac ttg ttg cat gtc cat	720
Ala Gly Val Ile Ala Ile Asp Leu Ala Lys Asp Leu Leu His Val His	
225 230 235 240	
aaa aat acg tat gct ctt gtg gtg agc aca gag aac atc act tat aac	768
Lys Asn Thr Tyr Ala Leu Val Val Ser Thr Glu Asn Ile Thr Tyr Asn	
245 250 255	
att tac gct ggt gat aat agg tcc atg atg gtt tca aat tgc ttg ttc	816
Ile Tyr Ala Gly Asp Asn Arg Ser Met Met Val Ser Asn Cys Leu Phe	
260 265 270	
cgt gtt ggt ggg gcc gct att ttg ctc tcc aac aag cct gga gat cgt	864
Arg Val Gly Gly Ala Ala Ile Leu Leu Ser Asn Lys Pro Gly Asp Arg	
275 280 285	
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Arg Arg Ser Lys Tyr Glu Leu Val His Thr Val Arg Thr His Thr Gly	
290 295 300	
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Ala Asp Asp Lys Ser Phe Arg Cys Val Gln Gln Gly Asp Asp Glu Asn	
305 310 315 320	
ggc aaa atc gga gtg agt ttg tcc aag gac ata acc gat gtt gct ggt	1008
Gly Lys Ile Gly Val Ser Leu Ser Lys Asp Ile Thr Asp Val Ala Gly	
325 330 335	
cga acg gtt aag aaa aac ata gca acg ttg ggt ccg ttg att ctt ccg	1056
Arg Thr Val Lys Lys Asn Ile Ala Thr Leu Gly Pro Leu Ile Leu Pro	
340 345 350	
tta agc gag aaa ctt ctt ttt ttc gtt acc ttc atg ggc aag aaa ctt	1104
Leu Ser Glu Lys Leu Leu Phe Phe Val Thr Phe Met Gly Lys Lys Leu	
355 360 365	
ttc aaa gat aaa atc aaa cat tac tac gtc ccg gat ttc aaa ctt gct	1152
Phe Lys Asp Lys Ile Lys His Tyr Tyr Val Pro Asp Phe Lys Leu Ala	
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Ile Asp His Phe Cys Ile His Ala Gly Gly Arg Ala Val Ile Asp Val	
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Leu Glu Lys Asn Leu Ala Leu Ala Pro Ile Asp Val Glu Ala Ser Arg	
405 410 415	
tca acg tta cat aga ttt gga aac act tca tct agc tca ata tgg tat	1296
Ser Thr Leu His Arg Phe Gly Asn Thr Ser Ser Ser Ser Ile Trp Tyr	
420 425 430	
gag ttg gca tac ata gaa gca aaa gga agg atg aag aaa ggt aat aaa	1344
Glu Leu Ala Tyr Ile Glu Ala Lys Gly Arg Met Lys Lys Gly Asn Lys	
435 440 445	

gtt tgg cag att gct tta ggg tca ggc ttt aag tgt aac agt gca gtt 1392
 Val Trp Gln Ile Ala Leu Gly Ser Gly Phe Lys Cys Asn Ser Ala Val
 450 455 460

tgg gtg gct cta aac aat gtc aaa gct tgc aca aat agt cct tgg gaa 1440
 Trp Val Ala Leu Asn Asn Val Lys Ala Ser Thr Asn Ser Pro Trp Glu
 465 470 475 480

cac tgc atc gac aga tac ccg gtc aaa att gat tct gat tca ggt aag 1488
 His Cys Ile Asp Arg Tyr Pro Val Lys Ile Asp Ser Asp Ser Gly Lys
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<210> 20

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<213> Artificial Sequence

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<223> 5' 114 amino acids from A. thaliana FAE1 (SEQ ID
 NO:2) and 3' 392 amino acids from B. napus
 elongase KCS (SEQ ID NO:4) having mutations at
 positions 91, 92 and 307; designated At114 L91C
 K92R G307D; hypothetical

<400> 20

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 20 25 30
 Ala Ser Arg Leu Thr Ile Asn Asp Leu His Asn Phe Leu Ser Tyr Leu
 35 40 45
 Gln His Asn Leu Ile Thr Val Thr Leu Leu Phe Ala Phe Thr Val Phe
 50 55 60
 Gly Leu Val Leu Tyr Ile Val Thr Arg Pro Asn Pro Val Tyr Leu Val
 65 70 75 80
 Asp Tyr Ser Cys Tyr Leu Pro Pro Pro His Cys Arg Val Ser Val Ser
 85 90 95
 Lys Val Met Asp Ile Phe Tyr Gln Ile Arg Lys Ala Asp Thr Ser Ser
 100 105 110
 Arg Asn Gly Thr Cys Asp Asn Ser Ser Trp Leu Asp Phe Leu Arg Lys
 115 120 125
 Ile Gln Glu Arg Ser Gly Leu Gly Asp Glu Thr His Gly Pro Glu Gly
 130 135 140
 Leu Leu Gln Val Pro Pro Arg Lys Thr Phe Ala Ala Ala Arg Glu Glu
 145 150 155 160
 Thr Glu Gln Val Ile Ile Gly Ala Leu Glu Asn Leu Phe Lys Asn Thr
 165 170 175
 Asn Val Asn Pro Lys Asp Ile Gly Ile Leu Val Val Asn Ser Ser Met
 180 185 190
 Phe Asn Pro Thr Pro Ser Leu Ser Ala Met Val Val Asn Thr Phe Lys
 195 200 205
 Leu Arg Ser Asn Val Arg Ser Phe Asn Leu Gly Gly Met Gly Cys Ser

210 215 220
 Ala Gly Val Ile Ala Ile Asp Leu Ala Lys Asp Leu Leu His Val His
 225 230 235 240
 Lys Asn Thr Tyr Ala Leu Val Val Ser Thr Glu Asn Ile Thr Tyr Asn
 245 250 255
 Ile Tyr Ala Gly Asp Asn Arg Ser Met Met Val Ser Asn Cys Leu Phe
 260 265 270
 Arg Val Gly Gly Ala Ala Ile Leu Leu Ser Asn Lys Pro Gly Asp Arg
 275 280 285
 Arg Arg Ser Lys Tyr Glu Leu Val His Thr Val Arg Thr His Thr Gly
 290 295 300
 Ala Asp Asp Lys Ser Phe Arg Cys Val Gln Gln Gly Asp Asp Glu Asn
 305 310 315 320
 Gly Lys Ile Gly Val Ser Leu Ser Lys Asp Ile Thr Asp Val Ala Gly
 325 330 335
 Arg Thr Val Lys Lys Asn Ile Ala Thr Leu Gly Pro Leu Ile Leu Pro
 340 345 350
 Leu Ser Glu Lys Leu Leu Phe Phe Val Thr Phe Met Gly Lys Lys Leu
 355 360 365
 Phe Lys Asp Lys Ile Lys His Tyr Tyr Val Pro Asp Phe Lys Leu Ala
 370 375 380
 Ile Asp His Phe Cys Ile His Ala Gly Gly Arg Ala Val Ile Asp Val
 385 390 395 400
 Leu Glu Lys Asn Leu Ala Leu Ala Pro Ile Asp Val Glu Ala Ser Arg
 405 410 415
 Ser Thr Leu His Arg Phe Gly Asn Thr Ser Ser Ser Ser Ile Trp Tyr
 420 425 430
 Glu Leu Ala Tyr Ile Glu Ala Lys Gly Arg Met Lys Lys Gly Asn Lys
 435 440 445
 Val Trp Gln Ile Ala Leu Gly Ser Gly Phe Lys Cys Asn Ser Ala Val
 450 455 460
 Trp Val Ala Leu Asn Asn Val Lys Ala Ser Thr Asn Ser Pro Trp Glu
 465 470 475 480
 His Cys Ile Asp Arg Tyr Pro Val Lys Ile Asp Ser Asp Ser Gly Lys
 485 490 495
 Ser Glu Thr Arg Val Gln Asn Gly Arg Ser
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<210> 21
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 <213> Artificial Sequence

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 <223> 5' 342 bp from A. thaliana FAE1 (SEQ ID NO:1) and
 3' 1179 bp from B. napus elongase KCS (SEQ ID
 NO:3) having mutations at positions 275 and 920;
 designated At114 K92R G307D; hypothetical

<221> CDS
 <222> (1)...(1518)

<400> 21
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 1 5 10 15

ttt ttc aac ctc tgt ttg ttc ccg tta acg gcg ttc ctc gcc gga aaa	96
Phe Phe Asn Leu Cys Leu Phe Pro Leu Thr Ala Phe Leu Ala Gly Lys	
20 25 30	
gcc tct cgg ctt acc ata aac gat ctc cac aac ttc ctt tcc tat ctc	144
Ala Ser Arg Leu Thr Ile Asn Asp Leu His Asn Phe Leu Ser Tyr Leu	
35 40 45	
caa cac aac ctt ata aca gta act tta ctc ttt gct ttc act gtt ttc	192
Gln His Asn Leu Ile Thr Val Thr Leu Leu Phe Ala Phe Thr Val Phe	
50 55 60	
ggg ttg gtt ctc tac atc gta acc cga ccc aat ccg gtt tat ctc gtt	240
Gly Leu Val Leu Tyr Ile Val Thr Arg Pro Asn Pro Val Tyr Leu Val	
65 70 75 80	
gac tac tcg tgt tac ctt ccg cca ccg cat ctc aga gtt agt gtc tct	288
Asp Tyr Ser Cys Tyr Leu Pro Pro Pro His Leu Arg Val Ser Val Ser	
85 90 95	
aaa gtc atg gat att ttc tac caa ata aga aaa gct gat act tct tca	336
Lys Val Met Asp Ile Phe Tyr Gln Ile Arg Lys Ala Asp Thr Ser Ser	
100 105 110	
cgg aac ggc acg tgt gat gat tcg tcg tgg ctt gac ttc ttg agg aag	384
Arg Asn Gly Thr Cys Asp Asp Ser Ser Trp Leu Asp Phe Leu Arg Lys	
115 120 125	
att caa gaa cgt tca ggt cta ggc gat gaa act cac ggg ccc gag ggg	432
Ile Gln Glu Arg Ser Gly Leu Gly Asp Glu Thr His Gly Pro Glu Gly	
130 135 140	
ctg ctt cag gtc cct ccc ccg aag act ttt gcg gcg gcg cgt gaa gag	480
Leu Leu Gln Val Pro Pro Arg Lys Thr Phe Ala Ala Ala Arg Glu Glu	
145 150 155 160	
acg gag caa gtt atc att ggt gcg cta gaa aat cta ttc aag aac acc	528
Thr Glu Gln Val Ile Ile Gly Ala Leu Glu Asn Leu Phe Lys Asn Thr	
165 170 175	
aac gtt aac cct aaa gat ata ggt ata ctt gtg gtg aac tca agc atg	576
Asn Val Asn Pro Lys Asp Ile Gly Ile Leu Val Val Asn Ser Ser Met	
180 185 190	
ttt aat cca act cca tcg ctc tcc gcg atg gtc gtt aac act ttc aag	624
Phe Asn Pro Thr Pro Ser Leu Ser Ala Met Val Val Asn Thr Phe Lys	
195 200 205	
ctc cga agc aac gta aga agc ttt aac ctt ggt ggc atg ggt tgt agt	672
Leu Arg Ser Asn Val Arg Ser Phe Asn Leu Gly Gly Met Gly Cys Ser	
210 215 220	
gcc ggc gtt ata gcc att gat cta gca aag gac ttg ttg cat gtc cat	720
Ala Gly Val Ile Ala Ile Asp Leu Ala Lys Asp Leu Leu His Val His	
225 230 235 240	
aaa aat acg tat gct ctt gtg gtg agc aca gag aac atc act tat aac	768

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Lys	Asn	Thr	Tyr	Ala	Leu	Val	Val	Ser	Thr	Glu	Asn	Ile	Thr	Tyr	Asn	
				245					250					255		
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Ile	Tyr	Ala	Gly	Asp	Asn	Arg	Ser	Met	Met	Val	Ser	Asn	Cys	Leu	Phe	
			260					265					270			
cgt	gtt	ggt	ggg	gcc	gct	att	ttg	ctc	tcc	aac	aag	cct	gga	gat	cgt	864
Arg	Val	Gly	Gly	Ala	Ala	Ile	Leu	Leu	Ser	Asn	Lys	Pro	Gly	Asp	Arg	
		275					280					285				
aga	cgg	tcc	aag	tac	gag	cta	gtt	cac	acg	gtt	cga	acg	cat	acc	gga	912
Arg	Arg	Ser	Lys	Tyr	Glu	Leu	Val	His	Thr	Val	Arg	Thr	His	Thr	Gly	
	290					295					300					
gct	gac	gac	aag	tct	ttt	cgt	tgc	gtg	caa	caa	gga	gac	gat	gag	aac	960
Ala	Asp	Asp	Lys	Ser	Phe	Arg	Cys	Val	Gln	Gln	Gly	Asp	Asp	Glu	Asn	
305					310					315					320	
ggc	aaa	atc	gga	gtg	agt	ttg	tcc	aag	gac	ata	acc	gat	gtt	gct	ggt	1008
Gly	Lys	Ile	Gly	Val	Ser	Leu	Ser	Lys	Asp	Ile	Thr	Asp	Val	Ala	Gly	
				325					330					335		
cga	acg	gtt	aag	aaa	aac	ata	gca	acg	ttg	ggt	ccg	ttg	att	ctt	ccg	1056
Arg	Thr	Val	Lys	Lys	Asn	Ile	Ala	Thr	Leu	Gly	Pro	Leu	Ile	Leu	Pro	
			340					345					350			
tta	agc	gag	aaa	ctt	ctt	ttt	ttc	gtt	acc	ttc	atg	ggc	aag	aaa	ctt	1104
Leu	Ser	Glu	Lys	Leu	Leu	Phe	Phe	Val	Thr	Phe	Met	Gly	Lys	Lys	Leu	
		355				360						365				
ttc	aaa	gat	aaa	atc	aaa	cat	tac	tac	gtc	ccg	gat	ttc	aaa	ctt	gct	1152
Phe	Lys	Asp	Lys	Ile	Lys	His	Tyr	Tyr	Val	Pro	Asp	Phe	Lys	Leu	Ala	
	370					375					380					
att	gac	cat	ttt	tgt	ata	cat	gcc	gga	ggc	aga	gcc	gtg	att	gat	gtg	1200
Ile	Asp	His	Phe	Cys	Ile	His	Ala	Gly	Gly	Arg	Ala	Val	Ile	Asp	Val	
385					390					395					400	
cta	gag	aag	aac	cta	gcc	cta	gca	ccg	atc	gat	gta	gag	gca	tca	aga	1248
Leu	Glu	Lys	Asn	Leu	Ala	Leu	Ala	Pro	Ile	Asp	Val	Glu	Ala	Ser	Arg	
			405						410					415		
tca	acg	tta	cat	aga	ttt	gga	aac	act	tca	tct	agc	tca	ata	tgg	tat	1296
Ser	Thr	Leu	His	Arg	Phe	Gly	Asn	Thr	Ser	Ser	Ser	Ser	Ile	Trp	Tyr	
			420					425					430			
gag	ttg	gca	tac	ata	gaa	gca	aaa	gga	agg	atg	aag	aaa	ggt	aat	aaa	1344
Glu	Leu	Ala	Tyr	Ile	Glu	Ala	Lys	Gly	Arg	Met	Lys	Lys	Gly	Asn	Lys	
		435					440					445				
gtt	tgg	cag	att	gct	tta	ggg	tca	ggc	ttt	aag	tgt	aac	agt	gca	gtt	1392
Val	Trp	Gln	Ile	Ala	Leu	Gly	Ser	Gly	Phe	Lys	Cys	Asn	Ser	Ala	Val	
	450					455					460					
tgg	gtg	gct	cta	aac	aat	gtc	aaa	gct	tcg	aca	aat	agt	cct	tgg	gaa	1440
Trp	Val	Ala	Leu	Asn	Asn	Val	Lys	Ala	Ser	Thr	Asn	Ser	Pro	Trp	Glu	

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<210> 22
<211> 506
<212> PRT
<213> Artificial Sequence
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<223> 5' 114 amino acids from A. thaliana FAE1 (SEQ ID NO:2) and 3' 392 amino acids from B. napus elongase KCS (SEQ ID NO:4) having mutations at positions 92 and 307; designated At114 K92R G307D; hypothetical

Met	Thr	Ser	Val	Asn	Val	Lys	Leu	Leu	Tyr	Arg	Tyr	Val	Leu	Thr	Asn
1				5					10					15	
Phe	Phe	Asn	Leu	Cys	Leu	Phe	Pro	Leu	Thr	Ala	Phe	Leu	Ala	Gly	Lys
			20					25					30		
Ala	Ser	Arg	Leu	Thr	Ile	Asn	Asp	Leu	His	Asn	Phe	Leu	Ser	Tyr	Leu
		35					40					45			
Gln	His	Asn	Leu	Ile	Thr	Val	Thr	Leu	Leu	Phe	Ala	Phe	Thr	Val	Phe
	50				55						60				
Gly	Leu	Val	Leu	Tyr	Ile	Val	Thr	Arg	Pro	Asn	Pro	Val	Tyr	Leu	Val
65					70					75					80
Asp	Tyr	Ser	Cys	Tyr	Leu	Pro	Pro	Pro	His	Leu	Arg	Val	Ser	Val	Ser
			85						90					95	
Lys	Val	Met	Asp	Ile	Phe	Tyr	Gln	Ile	Arg	Lys	Ala	Asp	Thr	Ser	Ser
			100					105					110		
Arg	Asn	Gly	Thr	Cys	Asp	Asp	Ser	Ser	Trp	Leu	Asp	Phe	Leu	Arg	Lys
		115					120					125			
Ile	Gln	Glu	Arg	Ser	Gly	Leu	Gly	Asp	Glu	Thr	His	Gly	Pro	Glu	Gly
	130					135					140				
Leu	Leu	Gln	Val	Pro	Pro	Arg	Lys	Thr	Phe	Ala	Ala	Ala	Arg	Glu	Glu
145					150					155					160
Thr	Glu	Gln	Val	Ile	Ile	Gly	Ala	Leu	Glu	Asn	Leu	Phe	Lys	Asn	Thr
				165					170					175	
Asn	Val	Asn	Pro	Lys	Asp	Ile	Gly	Ile	Leu	Val	Val	Asn	Ser	Ser	Met
			180					185					190		
Phe	Asn	Pro	Thr	Pro	Ser	Leu	Ser	Ala	Met	Val	Val	Asn	Thr	Phe	Lys
		195					200					205			
Leu	Arg	Ser	Asn	Val	Arg	Ser	Phe	Asn	Leu	Gly	Gly	Met	Gly	Cys	Ser
	210					215					220				
Ala	Gly	Val	Ile	Ala	Ile	Asp	Leu	Ala	Lys	Asp	Leu	Leu	His	Val	His
225					230					235					240
Lys	Asn	Thr	Tyr	Ala	Leu	Val	Val	Ser	Thr	Glu	Asn	Ile	Thr	Tyr	Asn
				245					250					255	
Ile	Tyr	Ala	Gly	Asp	Asn	Arg	Ser	Met	Met	Val	Ser	Asn	Cys	Leu	Phe

	260		265		270										
Arg	Val	Gly	Gly	Ala	Ala	Ile	Leu	Leu	Ser	Asn	Lys	Pro	Gly	Asp	Arg
	275						280					285			
Arg	Arg	Ser	Lys	Tyr	Glu	Leu	Val	His	Thr	Val	Arg	Thr	His	Thr	Gly
	290						295					300			
Ala	Asp	Asp	Lys	Ser	Phe	Arg	Cys	Val	Gln	Gln	Gly	Asp	Asp	Glu	Asn
305					310					315					320
Gly	Lys	Ile	Gly	Val	Ser	Leu	Ser	Lys	Asp	Ile	Thr	Asp	Val	Ala	Gly
			325						330					335	
Arg	Thr	Val	Lys	Lys	Asn	Ile	Ala	Thr	Leu	Gly	Pro	Leu	Ile	Leu	Pro
			340					345					350		
Leu	Ser	Glu	Lys	Leu	Leu	Phe	Phe	Val	Thr	Phe	Met	Gly	Lys	Lys	Leu
		355					360					365			
Phe	Lys	Asp	Lys	Ile	Lys	His	Tyr	Tyr	Val	Pro	Asp	Phe	Lys	Leu	Ala
	370					375					380				
Ile	Asp	His	Phe	Cys	Ile	His	Ala	Gly	Gly	Arg	Ala	Val	Ile	Asp	Val
385					390					395					400
Leu	Glu	Lys	Asn	Leu	Ala	Leu	Ala	Pro	Ile	Asp	Val	Glu	Ala	Ser	Arg
			405						410					415	
Ser	Thr	Leu	His	Arg	Phe	Gly	Asn	Thr	Ser	Ser	Ser	Ser	Ile	Trp	Tyr
			420					425					430		
Glu	Leu	Ala	Tyr	Ile	Glu	Ala	Lys	Gly	Arg	Met	Lys	Lys	Gly	Asn	Lys
		435					440					445			
Val	Trp	Gln	Ile	Ala	Leu	Gly	Ser	Gly	Phe	Lys	Cys	Asn	Ser	Ala	Val
	450					455					460				
Trp	Val	Ala	Leu	Asn	Asn	Val	Lys	Ala	Ser	Thr	Asn	Ser	Pro	Trp	Glu
465					470					475					480
His	Cys	Ile	Asp	Arg	Tyr	Pro	Val	Lys	Ile	Asp	Ser	Asp	Ser	Gly	Lys
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<210> 23

<211> 1521

<212> DNA

<213> Artificial Sequence

<220>

<223> 5' 762 bp from A. thaliana FAE1 (SEQ ID NO:1) and
 3' 759 bp from B. napus elongase KCS (SEQ ID
 NO:3); designated At254

<221> CDS

<222> (1)...(1518)

<400> 23

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Met	Thr	Ser	Val	Asn	Val	Lys	Leu	Leu	Tyr	Arg	Tyr	Val	Leu	Thr	Asn	
1				5					10					15		

ttt	ttc	aac	ctc	tgt	ttg	ttc	ccg	tta	acg	gcg	ttc	ctc	gcc	gga	aaa	96
Phe	Phe	Asn	Leu	Cys	Leu	Phe	Pro	Leu	Thr	Ala	Phe	Leu	Ala	Gly	Lys	
			20					25					30			

gcc	tct	cgg	ctt	acc	ata	aac	gat	ctc	cac	aac	ctc	ctt	tcc	tat	ctc	144
Ala	Ser	Arg	Leu	Thr	Ile	Asn	Asp	Leu	His	Asn	Leu	Leu	Ser	Tyr	Leu	
			35					40					45			

caa cac aac ctt ata aca gta act tta ctc ttt gct ttc act gtt ttc	192
Gln His Asn Leu Ile Thr Val Thr Leu Leu Phe Ala Phe Thr Val Phe	
50 55 60	
ggg ttg gtt ctc tac atc gta acc cga ccc aat ccg gtt tat ctc gtt	240
Gly Leu Val Leu Tyr Ile Val Thr Arg Pro Asn Pro Val Tyr Leu Val	
65 70 75 80	
gac tac tcg tgt tac ctt cca cca ccg cat ctc aaa gtt agt gtc tct	288
Asp Tyr Ser Cys Tyr Leu Pro Pro Pro His Leu Lys Val Ser Val Ser	
85 90 95	
aaa gtc atg gat att ttc tac caa ata aga aaa gct gat act tct tca	336
Lys Val Met Asp Ile Phe Tyr Gln Ile Arg Lys Ala Asp Thr Ser Ser	
100 105 110	
cgg aac gtg gca tgt gat gat ccg tcc tcg ctc gat ttc ctg agg aag	384
Arg Asn Val Ala Cys Asp Asp Pro Ser Ser Leu Asp Phe Leu Arg Lys	
115 120 125	
att caa gag cgt tca ggt cta ggt gat gag acg tac agt cct gag gga	432
Ile Gln Glu Arg Ser Gly Leu Gly Asp Glu Thr Tyr Ser Pro Glu Gly	
130 135 140	
ctc att cac gta cca ccg cgg aag act ttt gca gcg tca cgt gaa gag	480
Leu Ile His Val Pro Arg Lys Thr Phe Ala Ala Ser Arg Glu Glu	
145 150 155 160	
aca gag aag gtt atc atc ggt gcg ctc gaa aat cta ttc gag aac acc	528
Thr Glu Lys Val Ile Ile Gly Ala Leu Glu Asn Leu Phe Glu Asn Thr	
165 170 175	
aaa gtt aac cct aga gag att ggt ata ctt gtg gtg aac tca agc atg	576
Lys Val Asn Pro Arg Glu Ile Gly Ile Leu Val Val Asn Ser Ser Met	
180 185 190	
ttt aat cca act cct tcg cta tcc gct atg gtc gtt aat act ttc aag	624
Phe Asn Pro Thr Pro Ser Leu Ser Ala Met Val Val Asn Thr Phe Lys	
195 200 205	
ctc cga agc aac atc aaa agc ttt aat cta gga gga atg ggt tgt agt	672
Leu Arg Ser Asn Ile Lys Ser Phe Asn Leu Gly Gly Met Gly Cys Ser	
210 215 220	
gct ggt gtt att gcc att gat ttg gct aaa gac ttg ttg cat gtt cat	720
Ala Gly Val Ile Ala Ile Asp Leu Ala Lys Asp Leu Leu His Val His	
225 230 235 240	
aaa aac act tat gct ctc gtg gtg agc aca gag aac atc act tat aac	768
Lys Asn Thr Tyr Ala Leu Val Val Ser Thr Glu Asn Ile Thr Tyr Asn	
245 250 255	
att tac gct ggt gat aat agg tcc atg atg gtt tca aat tgc ttg ttc	816
Ile Tyr Ala Gly Asp Asn Arg Ser Met Met Val Ser Asn Cys Leu Phe	
260 265 270	

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Ser Glu Thr Arg Val Pro Asn Gly Arg Ser
500 505

<210> 24
<211> 506
<212> PRT
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<220>
<223> 5' 254 amino acids from A. thaliana FAE1 (SEQ ID NO:2) and 3' 252 amino acids from B. napus elongase KCS (SEQ ID NO:4); designated At254

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Phe Phe Asn Leu Cys Leu Phe Pro Leu Thr Ala Phe Leu Ala Gly Lys
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Ala Ser Arg Leu Thr Ile Asn Asp Leu His Asn Leu Leu Ser Tyr Leu
35 40 45
Gln His Asn Leu Ile Thr Val Thr Leu Leu Phe Ala Phe Thr Val Phe
50 55 60
Gly Leu Val Leu Tyr Ile Val Thr Arg Pro Asn Pro Val Tyr Leu Val
65 70 75 80
Asp Tyr Ser Cys Tyr Leu Pro Pro Pro His Leu Lys Val Ser Val Ser
85 90 95
Lys Val Met Asp Ile Phe Tyr Gln Ile Arg Lys Ala Asp Thr Ser Ser
100 105 110
Arg Asn Val Ala Cys Asp Asp Pro Ser Ser Leu Asp Phe Leu Arg Lys
115 120 125
Ile Gln Glu Arg Ser Gly Leu Gly Asp Glu Thr Tyr Ser Pro Glu Gly
130 135 140
Leu Ile His Val Pro Pro Arg Lys Thr Phe Ala Ala Ser Arg Glu Glu
145 150 155 160
Thr Glu Lys Val Ile Ile Gly Ala Leu Glu Asn Leu Phe Glu Asn Thr
165 170 175
Lys Val Asn Pro Arg Glu Ile Gly Ile Leu Val Val Asn Ser Ser Met
180 185 190
Phe Asn Pro Thr Pro Ser Leu Ser Ala Met Val Val Asn Thr Phe Lys
195 200 205
Leu Arg Ser Asn Ile Lys Ser Phe Asn Leu Gly Gly Met Gly Cys Ser
210 215 220
Ala Gly Val Ile Ala Ile Asp Leu Ala Lys Asp Leu Leu His Val His
225 230 235 240
Lys Asn Thr Tyr Ala Leu Val Val Ser Thr Glu Asn Ile Thr Tyr Asn
245 250 255
Ile Tyr Ala Gly Asp Asn Arg Ser Met Met Val Ser Asn Cys Leu Phe
260 265 270
Arg Val Gly Gly Ala Ala Ile Leu Leu Ser Asn Lys Pro Gly Asp Arg
275 280 285
Arg Arg Ser Lys Tyr Glu Leu Val His Thr Val Arg Thr His Thr Gly
290 295 300
Ala Asp Gly Lys Ser Phe Arg Cys Val Gln Gln Gly Asp Asp Glu Asn
305 310 315 320
Gly Lys Ile Gly Val Ser Leu Ser Lys Asp Ile Thr Asp Val Ala Gly
325 330 335

Arg Thr Val Lys Lys Asn Ile Ala Thr Leu Gly Pro Leu Ile Leu Pro
 340 345 350
 Leu Ser Glu Lys Leu Leu Phe Phe Val Thr Phe Met Gly Lys Lys Leu
 355 360 365
 Phe Lys Asp Lys Ile Lys His Tyr Tyr Val Pro Asp Phe Lys Leu Ala
 370 375 380
 Ile Asp His Phe Cys Ile His Ala Gly Gly Arg Ala Val Ile Asp Val
 385 390 395 400
 Leu Glu Lys Asn Leu Ala Leu Ala Pro Ile Asp Val Glu Ala Ser Arg
 405 410 415
 Ser Thr Leu His Arg Phe Gly Asn Thr Ser Ser Ser Ser Ile Trp Tyr
 420 425 430
 Glu Leu Ala Tyr Ile Glu Ala Lys Gly Arg Met Lys Lys Gly Asn Lys
 435 440 445
 Val Trp Gln Ile Ala Leu Gly Ser Gly Phe Lys Cys Asn Ser Ala Val
 450 455 460
 Trp Val Ala Leu Asn Asn Val Lys Ala Ser Thr Asn Ser Pro Trp Glu
 465 470 475 480
 His Cys Ile Asp Arg Tyr Pro Val Lys Ile Asp Ser Asp Ser Gly Lys
 485 490 495
 Ser Glu Thr Arg Val Pro Asn Gly Arg Ser
 500 505

<210> 25

<211> 1521

<212> DNA

<213> Artificial Sequence

<220>

<223> 5' 519 bp from A. thaliana FAE1 (SEQ ID NO:1) and
 3' 1002 bp from B. napus elongase KCS (SEQ ID
 NO:3); designated At173

<221> CDS

<222> (1) ... (1518)

<400> 25

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 Met Thr Ser Val Asn Val Lys Leu Leu Tyr Arg Tyr Val Leu Thr Asn
 1 5 10 15

ttt ttc aac ctc tgt ttg ttc ccg tta acg gcg ttc ctc gcc gga aaa 96
 Phe Phe Asn Leu Cys Leu Phe Pro Leu Thr Ala Phe Leu Ala Gly Lys
 20 25 30

gcc tct cgg ctt acc ata aac gat ctc cac aac ttc ctt tcc tat ctc 144
 Ala Ser Arg Leu Thr Ile Asn Asp Leu His Asn Phe Leu Ser Tyr Leu
 35 40 45

caa cac aac ctt ata aca gta act tta ctc ttt gct ttc act gtt ttc 192
 Gln His Asn Leu Ile Thr Val Thr Leu Leu Phe Ala Phe Thr Val Phe
 50 55 60

ggt ttg gtt ctc tac atc gta acc cga ccc aat ccg gtt tat ctc gtt 240
 Gly Leu Val Leu Tyr Ile Val Thr Arg Pro Asn Pro Val Tyr Leu Val
 65 70 75 80

gac tac tcg tgt tac ctt cca cca ccg cat ctc aaa gtt agt gtc tct Asp Tyr Ser Cys Tyr Leu Pro Pro Pro His Leu Lys Val Ser Val Ser	288
85 90 95	
aaa gtc atg gat att ttc tac caa ata aga aaa gct gat act tct tca Lys Val Met Asp Ile Phe Tyr Gln Ile Arg Lys Ala Asp Thr Ser Ser	336
100 105 110	
cgg aac gtg gca tgt gat gat ccg tcc tcg ctc gat ttc ctg agg aag Arg Asn Val Ala Cys Asp Asp Pro Ser Ser Leu Asp Phe Leu Arg Lys	384
115 120 125	
att caa gag cgt tca ggt cta ggt gat gag acg tac agt cct gag gga Ile Gln Glu Arg Ser Gly Leu Gly Asp Glu Thr Tyr Ser Pro Glu Gly	432
130 135 140	
ctc att cac gta cca ccg cgg aag act ttt gca gcg tca cgt gaa gag Leu Ile His Val Pro Pro Arg Lys Thr Phe Ala Ala Ser Arg Glu Glu	480
145 150 155 160	
aca gag aag gtt atc atc ggt gcg ctc gaa aat cta ttc aag aac acc Thr Glu Lys Val Ile Ile Gly Ala Leu Glu Asn Leu Phe Lys Asn Thr	528
165 170 175	
aac gtt aac cct aaa gat ata ggt ata ctt gtg gtg aac tca agc atg Asn Val Asn Pro Lys Asp Ile Gly Ile Leu Val Val Asn Ser Ser Met	576
180 185 190	
ttt aat cca act cca tcg ctc tcc gcg atg gtc gtt aac act ttc aag Phe Asn Pro Thr Pro Ser Leu Ser Ala Met Val Val Asn Thr Phe Lys	624
195 200 205	
ctc cga agc aac gta aga agc ttt aac ctt ggt ggc atg ggt tgt agt Leu Arg Ser Asn Val Arg Ser Phe Asn Leu Gly Gly Met Gly Cys Ser	672
210 215 220	
gcc gcc gtt ata gcc att gat cta gca aag gac ttg ttg cat gtc cat Ala Gly Val Ile Ala Ile Asp Leu Ala Lys Asp Leu Leu His Val His	720
225 230 235 240	
aaa aat acg tat gct ctt gtg gtg agc aca gag aac atc act tat aac Lys Asn Thr Tyr Ala Leu Val Val Ser Thr Glu Asn Ile Thr Tyr Asn	768
245 250 255	
att tac gct ggt gat aat agg tcc atg atg gtt tca aat tgc ttg ttc Ile Tyr Ala Gly Asp Asn Arg Ser Met Met Val Ser Asn Cys Leu Phe	816
260 265 270	
cgt gtt ggt ggg gcc gct att ttg ctc tcc aac aag cct gga gat cgt Arg Val Gly Gly Ala Ala Ile Leu Leu Ser Asn Lys Pro Gly Asp Arg	864
275 280 285	
aga cgg tcc aag tac gag cta gtt cac acg gtt cga acg cat acc gga Arg Arg Ser Lys Tyr Glu Leu Val His Thr Val Arg Thr His Thr Gly	912
290 295 300	
gct gac gcc aag tct ttt cgt tgc gtg caa caa gga gac gat gag aac	960

Ala Asp Gly Lys Ser Phe Arg Cys Val Gln Gln Gly Asp Asp Glu Asn	
305 310 315 320	
ggc aaa atc gga gtg agt ttg tcc aag gac ata acc gat gtt gct ggt	1008
Gly Lys Ile Gly Val Ser Leu Ser Lys Asp Ile Thr Asp Val Ala Gly	
325 330 335	
cga acg gtt aag aaa aac ata gca acg ttg ggt ccg ttg att ctt ccg	1056
Arg Thr Val Lys Lys Asn Ile Ala Thr Leu Gly Pro Leu Ile Leu Pro	
340 345 350	
tta agc gag aaa ctt ctt ttt ttc gtt acc ttc atg ggc aag aaa ctt	1104
Leu Ser Glu Lys Leu Leu Phe Phe Val Thr Phe Met Gly Lys Lys Leu	
355 360 365	
ttc aaa gat aaa atc aaa cat tac tac gtc ccg gat ttc aaa ctt gct	1152
Phe Lys Asp Lys Ile Lys His Tyr Tyr Val Pro Asp Phe Lys Leu Ala	
370 375 380	
att gac cat ttt tgt ata cat gcc gga ggc aga gcc gtg att gat gtg	1200
Ile Asp His Phe Cys Ile His Ala Gly Gly Arg Ala Val Ile Asp Val	
385 390 395 400	
cta gag aag aac cta gcc cta gca ccg atc gat gta gag gca tca aga	1248
Leu Glu Lys Asn Leu Ala Leu Ala Pro Ile Asp Val Glu Ala Ser Arg	
405 410 415	
tca acg tta cat aga ttt gga aac act tca tct agc tca ata tgg tat	1296
Ser Thr Leu His Arg Phe Gly Asn Thr Ser Ser Ser Ser Ile Trp Tyr	
420 425 430	
gag ttg gca tac ata gaa gca aaa gga agg atg aag aaa ggt aat aaa	1344
Glu Leu Ala Tyr Ile Glu Ala Lys Gly Arg Met Lys Lys Gly Asn Lys	
435 440 445	
gtt tgg cag att gct tta ggg tca ggc ttt aag tgt aac agt gca gtt	1392
Val Trp Gln Ile Ala Leu Gly Ser Gly Phe Lys Cys Asn Ser Ala Val	
450 455 460	
tgg gtg gct cta aac aat gtc aaa gct tcg aca aat agt cct tgg gaa	1440
Trp Val Ala Leu Asn Asn Val Lys Ala Ser Thr Asn Ser Pro Trp Glu	
465 470 475 480	
cac tgc atc gac aga tac ccg gtc aaa att gat tct gat tca ggt aag	1488
His Cys Ile Asp Arg Tyr Pro Val Lys Ile Asp Ser Asp Ser Gly Lys	
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<210> 26

<211> 506

<212> PRT

<213> Artificial Sequence

<223> 5' 173 amino acids from *A. thaliana* FAE1 (SEQ ID NO:2) and 3' 333 amino acids from *B. napus* elongase KCS (SEQ ID NO:4); designated At173

$$\langle 222 \rangle \quad (0) \dots (0)$$

<223> Xaa = Pro or Gln

Met	Thr	Ser	Val	Asn	Val	Lys	Leu	Leu	Tyr	Arg	Tyr	Val	Leu	Thr	Asn
1				5					10					15	
Phe	Phe	Asn	Leu	Cys	Leu	Phe	Pro	Leu	Thr	Ala	Phe	Leu	Ala	Gly	Lys
			20					25				30			
Ala	Ser	Arg	Leu	Thr	Ile	Asn	Asp	Leu	His	Asn	Phe	Leu	Ser	Tyr	Leu
		35					40				45				
Gln	His	Asn	Leu	Ile	Thr	Val	Thr	Leu	Leu	Phe	Ala	Phe	Thr	Val	Phe
	50				55					60					
Gly	Leu	Val	Leu	Tyr	Ile	Val	Thr	Arg	Pro	Asn	Pro	Val	Tyr	Leu	Val
65				70					75						80
Asp	Tyr	Ser	Cys	Tyr	Leu	Pro	Pro	Pro	His	Leu	Lys	Val	Ser	Val	Ser
			85						90				95		
Lys	Val	Met	Asp	Ile	Phe	Tyr	Gln	Ile	Arg	Lys	Ala	Asp	Thr	Ser	Ser
			100					105				110			
Arg	Asn	Val	Ala	Cys	Asp	Asp	Pro	Ser	Ser	Leu	Asp	Phe	Leu	Arg	Lys
		115					120				125				
Ile	Gln	Glu	Arg	Ser	Gly	Leu	Gly	Asp	Glu	Thr	Tyr	Ser	Pro	Glu	Gly
	130				135					140					
Leu	Ile	His	Val	Pro	Pro	Arg	Lys	Thr	Phe	Ala	Ala	Ser	Arg	Glu	Glu
145				150					155					160	
Thr	Glu	Lys	Val	Ile	Ile	Gly	Ala	Leu	Glu	Asn	Leu	Phe	Lys	Asn	Thr
			165					170					175		
Asn	Val	Asn	Pro	Lys	Asp	Ile	Gly	Ile	Leu	Val	Val	Asn	Ser	Ser	Met
			180				185					190			
Phe	Asn	Pro	Thr	Pro	Ser	Leu	Ser	Ala	Met	Val	Val	Asn	Thr	Phe	Lys
		195					200				205				
Leu	Arg	Ser	Asn	Val	Arg	Ser	Phe	Asn	Leu	Gly	Gly	Met	Gly	Cys	Ser
	210					215				220					
Ala	Gly	Val	Ile	Ala	Ile	Asp	Leu	Ala	Lys	Asp	Leu	Leu	His	Val	His
225				230					235					240	
Lys	Asn	Thr	Tyr	Ala	Leu	Val	Val	Ser	Thr	Glu	Asn	Ile	Thr	Tyr	Asn
			245					250					255		
Ile	Tyr	Ala	Gly	Asp	Asn	Arg	Ser	Met	Met	Val	Ser	Asn	Cys	Leu	Phe
		260					265					270			
Arg	Val	Gly	Gly	Ala	Ala	Ile	Leu	Leu	Ser	Asn	Lys	Pro	Gly	Asp	Arg
		275				280					285				
Arg	Arg	Ser	Lys	Tyr	Glu	Leu	Val	His	Thr	Val	Arg	Thr	His	Thr	Gly
	290				295					300					
Ala	Asp	Gly	Lys	Ser	Phe	Arg	Cys	Val	Gln	Gln	Gly	Asp	Asp	Glu	Asn
305				310					315					320	
Gly	Lys	Ile	Gly	Val	Ser	Leu	Ser	Lys	Asp	Ile	Thr	Asp	Val	Ala	Gly
			325					330					335		
Arg	Thr	Val	Lys	Lys	Asn	Ile	Ala	Thr	Leu	Gly	Pro	Leu	Ile	Leu	Pro
		340					345					350			
Leu	Ser	Glu	Lys	Leu</											

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      370              375              380
Ile Asp His Phe Cys Ile His Ala Gly Gly Arg Ala Val Ile Asp Val
385              390              395              400
Leu Glu Lys Asn Leu Ala Leu Ala Pro Ile Asp Val Glu Ala Ser Arg
      405              410              415
Ser Thr Leu His Arg Phe Gly Asn Thr Ser Ser Ser Ser Ile Trp Tyr
      420              425              430
Glu Leu Ala Tyr Ile Glu Ala Lys Gly Arg Met Lys Lys Gly Asn Lys
      435              440              445
Val Trp Gln Ile Ala Leu Gly Ser Gly Phe Lys Cys Asn Ser Ala Val
      450              455              460
Trp Val Ala Leu Asn Asn Val Lys Ala Ser Thr Asn Ser Pro Trp Glu
465              470              475              480
His Cys Ile Asp Arg Tyr Pro Val Lys Ile Asp Ser Asp Ser Gly Lys
      485              490              495
Ser Glu Thr Arg Val Xaa Asn Gly Arg Ser
      500              505

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<210> 27
<211> 1521
<212> DNA
<213> Artificial Sequence

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<220>
<223> 5' 528 bp from B. napus elongase KCS (SEQ ID NO:3)
      and 3' 993 bp from A. thaliana FAEl (SEQ ID NO:1);
      designated Bn176

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<221> CDS
<222> (1)...(1518)

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<400> 27
atg acg tcc att aac gta aag ctc ctt tac cat tac gtc ata acc aac      48
Met Thr Ser Ile Asn Val Lys Leu Leu Tyr His Tyr Val Ile Thr Asn
  1              5              10              15

ctt ttc aac ctt tgc ttc ttt ccg tta acg gcg atc gtc gcc gga aaa      96
Leu Phe Asn Leu Cys Phe Phe Pro Leu Thr Ala Ile Val Ala Gly Lys
      20              25              30

gcc tat cgg ctt acc ata gac gat ctt cac cac tta tac tat tcc tat      144
Ala Tyr Arg Leu Thr Ile Asp Asp Leu His His Leu Tyr Tyr Ser Tyr
      35              40              45

ctc caa cac aac ctc ata acc atc gct cca ctc ttt gcc ttc acc gtt      192
Leu Gln His Asn Leu Ile Thr Ile Ala Pro Leu Phe Ala Phe Thr Val
      50              55              60

ttc ggt tcg gtt ctc tac atc gca acc ccg ccc aaa ccg gtt tac ctc      240
Phe Gly Ser Val Leu Tyr Ile Ala Thr Arg Pro Lys Pro Val Tyr Leu
      65              70              75              80

gtt gag tac tca tgc tac ctt cca cca acg cat tgt aga tca agt atc      288
Val Glu Tyr Ser Cys Tyr Leu Pro Pro Thr His Cys Arg Ser Ser Ile
      85              90              95

tcc aag gtc atg gat atc ttt tat caa gta aga aaa gct gat cct tct      336

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Ser Lys Val Met Asp Ile Phe Tyr Gln Val Arg Lys Ala Asp Pro Ser
 100 105 110

cgg aac ggc acg tgc gat gac tcg tcg tgg ctt gac ttc ttg agg aag 384
 Arg Asn Gly Thr Cys Asp Asp Ser Ser Trp Leu Asp Phe Leu Arg Lys
 115 120 125

att caa gaa cgt tca ggt cta ggc gat gaa act cac ggg ccc gag ggg 432
 Ile Gln Glu Arg Ser Gly Leu Gly Asp Glu Thr His Gly Pro Glu Gly
 130 135 140

ctg ctt cag gtc cct ccc cgg aag act ttt gcg gcg gcg cgt gaa gag 480
 Leu Leu Gln Val Pro Pro Arg Lys Thr Phe Ala Ala Ala Arg Glu Glu
 145 150 155 160

acg gag caa gtt atc att ggt gcg cta gaa aat cta ttc aag aac acc 528
 Thr Glu Gln Val Ile Ile Gly Ala Leu Glu Asn Leu Phe Lys Asn Thr
 165 170 175

aaa gtt aac cct aga gag att ggt ata ctt gtg gtg aac tca agc atg 576
 Lys Val Asn Pro Arg Glu Ile Gly Ile Leu Val Val Asn Ser Ser Met
 180 185 190

ttt aat cca act cct tcg cta tcc gct atg gtc gtt aat act ttc aag 624
 Phe Asn Pro Thr Pro Ser Leu Ser Ala Met Val Val Asn Thr Phe Lys
 195 200 205

ctc cga agc aac atc aaa agc ttt aat cta gga gga atg ggt tgt agt 672
 Leu Arg Ser Asn Ile Lys Ser Phe Asn Leu Gly Gly Met Gly Cys Ser
 210 215 220

gct ggt gtt att gcc att gat ttg gct aaa gac ttg ttg cat gtt cat 720
 Ala Gly Val Ile Ala Ile Asp Leu Ala Lys Asp Leu Leu His Val His
 225 230 235 240

aaa aac act tat gct ctt gtg gtg agc act gag aac atc aca caa ggc 768
 Lys Asn Thr Tyr Ala Leu Val Val Ser Thr Glu Asn Ile Thr Gln Gly
 245 250 255

att tat gct gga gaa aat aga tca atg atg gtt agc aat tgc ttg ttt 816
 Ile Tyr Ala Gly Glu Asn Arg Ser Met Met Val Ser Asn Cys Leu Phe
 260 265 270

cgt gtt ggt ggg gcc gcg att ttg ctc tct aac aag tcg gga gac cgg 864
 Arg Val Gly Gly Ala Ala Ile Leu Leu Ser Asn Lys Ser Gly Asp Arg
 275 280 285

aga cgg tcc aag tac aag cta gtt cac acg gtc cga acg cat act gga 912
 Arg Arg Ser Lys Tyr Lys Leu Val His Thr Val Arg Thr His Thr Gly
 290 295 300

gct gat gac aag tct ttt cga tgt gtg caa caa gaa gat gat gag agc 960
 Ala Asp Asp Lys Ser Phe Arg Cys Val Gln Gln Glu Asp Asp Glu Ser
 305 310 315 320

ggc aaa atc gga gtt tgt ctg tca aag gac ata acc aat gtt gcg ggg 1008
 Gly Lys Ile Gly Val Cys Leu Ser Lys Asp Ile Thr Asn Val Ala Gly

100 110 120 130 140 150 160 170 180 190 200 210 220 230 240 250 260 270 280 290 300 310 320

	325	330	335	
aca aca ctt acg aaa aat ata gca aca ttg ggt ccg ttg att ctt cct				1056
Thr Thr Leu Thr Lys Asn Ile Ala Thr Leu Gly Pro Leu Ile Leu Pro				
	340	345	350	
tta agc gaa aag ttt ctt ttt ttc gct acc ttc gtc gcc aag aaa ctt				1104
Leu Ser Glu Lys Phe Leu Phe Phe Ala Thr Phe Val Ala Lys Lys Leu				
	355	360	365	
cta aag gat aaa atc aag cat tac tat gtt ccg gat ttc aag ctt gct				1152
Leu Lys Asp Lys Ile Lys His Tyr Tyr Val Pro Asp Phe Lys Leu Ala				
	370	375	380	
gtt gac cat ttc tgt att cat gcc gga ggc aga gcc gtg atc gat gag				1200
Val Asp His Phe Cys Ile His Ala Gly Gly Arg Ala Val Ile Asp Glu				
	385	390	395	400
cta gag aag aac tta gga cta tcg ccg atc gat gtg gag gca tct aga				1248
Leu Glu Lys Asn Leu Gly Leu Ser Pro Ile Asp Val Glu Ala Ser Arg				
	405	410	415	
tca acg tta cat aga ttt ggg aat act tca tct agc tca att tgg tat				1296
Ser Thr Leu His Arg Phe Gly Asn Thr Ser Ser Ser Ser Ile Trp Tyr				
	420	425	430	
gaa tta gca tac ata gag gca aag gga aga atg aag aaa ggg aat aaa				1344
Glu Leu Ala Tyr Ile Glu Ala Lys Gly Arg Met Lys Lys Gly Asn Lys				
	435	440	445	
gct tgg cag att gct tta gga tca ggg ttt aag tgt aat agt gcg gtt				1392
Ala Trp Gln Ile Ala Leu Gly Ser Gly Phe Lys Cys Asn Ser Ala Val				
	450	455	460	
tgg gtg gct cta cgc aat gtc aag gca tcg gca aat agt cct tgg caa				1440
Trp Val Ala Leu Arg Asn Val Lys Ala Ser Ala Asn Ser Pro Trp Gln				
	465	470	475	480
cat tgc atc gat aga tat ccg gtt aaa att gat tct gat ttg tca aag				1488
His Cys Ile Asp Arg Tyr Pro Val Lys Ile Asp Ser Asp Leu Ser Lys				
	485	490	495	
tca aag act cat gtc caa aac ggt cgg tcc taa				1521
Ser Lys Thr His Val Gln Asn Gly Arg Ser				
	500	505		

<210> 28
 <211> 506
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 5' 176 amino acids from B. napus elongase KCS (SEQ
 ID NO:4) and 3' 330 amino acids from A. thaliana
 FAE1 (SEQ ID NO:2); designated Bn176

<400> 28

Met	Thr	Ser	Ile	Asn	Val	Lys	Leu	Leu	Tyr	His	Tyr	Val	Ile	Thr	Asn
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Leu	Phe	Asn	Leu	Cys	Phe	Phe	Pro	Leu	Thr	Ala	Ile	Val	Ala	Gly	Lys
		20						25					30		
Ala	Tyr	Arg	Leu	Thr	Ile	Asp	Asp	Leu	His	His	Leu	Tyr	Tyr	Ser	Tyr
		35				40						45			
Leu	Gln	His	Asn	Leu	Ile	Thr	Ile	Ala	Pro	Leu	Phe	Ala	Phe	Thr	Val
	50					55					60				
Phe	Gly	Ser	Val	Leu	Tyr	Ile	Ala	Thr	Arg	Pro	Lys	Pro	Val	Tyr	Leu
65					70					75					80
Val	Glu	Tyr	Ser	Cys	Tyr	Leu	Pro	Pro	Thr	His	Cys	Arg	Ser	Ser	Ile
				85					90					95	
Ser	Lys	Val	Met	Asp	Ile	Phe	Tyr	Gln	Val	Arg	Lys	Ala	Asp	Pro	Ser
			100					105					110		
Arg	Asn	Gly	Thr	Cys	Asp	Asp	Ser	Ser	Trp	Leu	Asp	Phe	Leu	Arg	Lys
		115					120					125			
Ile	Gln	Glu	Arg	Ser	Gly	Leu	Gly	Asp	Glu	Thr	His	Gly	Pro	Glu	Gly
	130					135					140				
Leu	Leu	Gln	Val	Pro	Pro	Arg	Lys	Thr	Phe	Ala	Ala	Ala	Arg	Glu	Glu
145					150					155					160
Thr	Glu	Gln	Val	Ile	Ile	Gly	Ala	Leu	Glu	Asn	Leu	Phe	Lys	Asn	Thr
				165					170					175	
Lys	Val	Asn	Pro	Arg	Glu	Ile	Gly	Ile	Leu	Val	Val	Asn	Ser	Ser	Met
			180				185						190		
Phe	Asn	Pro	Thr	Pro	Ser	Leu	Ser	Ala	Met	Val	Val	Asn	Thr	Phe	Lys
		195					200					205			
Leu	Arg	Ser	Asn	Ile	Lys	Ser	Phe	Asn	Leu	Gly	Gly	Met	Gly	Cys	Ser
	210				215						220				
Ala	Gly	Val	Ile	Ala	Ile	Asp	Leu	Ala	Lys	Asp	Leu	Leu	His	Val	His
225					230					235					240
Lys	Asn	Thr	Tyr	Ala	Leu	Val	Val	Ser	Thr	Glu	Asn	Ile	Thr	Gln	Gly
				245					250					255	
Ile	Tyr	Ala	Gly	Glu	Asn	Arg	Ser	Met	Met	Val	Ser	Asn	Cys	Leu	Phe
			260					265					270		
Arg	Val	Gly	Gly	Ala	Ala	Ile	Leu	Leu	Ser	Asn	Lys	Ser	Gly	Asp	Arg
		275					280					285			
Arg	Arg	Ser	Lys	Tyr	Lys	Leu	Val	His	Thr	Val	Arg	Thr	His	Thr	Gly
		290				295					300				
Ala	Asp	Asp	Lys	Ser	Phe	Arg	Cys	Val	Gln	Gln	Glu	Asp	Asp	Glu	Ser
305					310					315					320
Gly	Lys	Ile	Gly	Val	Cys	Leu	Ser	Lys	Asp	Ile	Thr	Asn	Val	Ala	Gly
				325					330					335	
Thr	Thr	Leu	Thr	Lys	Asn	Ile	Ala	Thr	Leu	Gly	Pro	Leu	Ile	Leu	Pro
			340					345					350		
Leu	Ser	Glu	Lys	Phe	Leu	Phe	Phe	Ala	Thr	Phe	Val	Ala	Lys	Lys	Leu
		355					360					365			
Leu	Lys	Asp	Lys	Ile	Lys	His	Tyr	Tyr	Val	Pro	Asp	Phe	Lys	Leu	Ala
	370					375					380				
Val	Asp	His	Phe	Cys	Ile	His	Ala	Gly	Gly	Arg	Ala	Val	Ile	Asp	Glu
385					390					395					400
Leu	Glu	Lys	Asn	Leu	Gly	Leu	Ser	Pro	Ile	Asp	Val	Glu	Ala	Ser	Arg
				405					410					415	
Ser	Thr	Leu	His	Arg	Phe	Gly	Asn	Thr	Ser	Ser	Ser	Ser	Ile	Trp	Tyr
			420					425					430		
Glu	Leu	Ala	Tyr	Ile	Glu	Ala	Lys	Gly	Arg	Met	Lys	Lys	Gly	Asn	Lys
		435					440						445		

Ala Trp Gln Ile Ala Leu Gly Ser Gly Phe Lys Cys Asn Ser Ala Val
 450 455 460
 Trp Val Ala Leu Arg Asn Val Lys Ala Ser Ala Asn Ser Pro Trp Gln
 465 470 475 480
 His Cys Ile Asp Arg Tyr Pro Val Lys Ile Asp Ser Asp Leu Ser Lys
 485 490 495
 Ser Lys Thr His Val Gln Asn Gly Arg Ser
 500 505

<210> 29

<211> 1521

<212> DNA

<213> Artificial Sequence

<220>

<223> 5' 1197 bp from A. thaliana FAE1 (SEQ ID NO:1) and
 3' 324 bp from B. napus elongase KCS (SEQ ID
 NO:3); designated At399

<221> CDS

<222> (1)...(1518)

<400> 29

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Met	Thr	Ser	Val	Asn	Val	Lys	Leu	Leu	Tyr	Arg	Tyr	Val	Leu	Thr	Asn	
1				5					10				15			

ttt	ttc	aac	ctc	tgt	ttg	ttc	cgg	tta	acg	gcg	ttc	ctc	gcc	gga	aaa	96
Phe	Phe	Asn	Leu	Cys	Leu	Phe	Pro	Leu	Thr	Ala	Phe	Leu	Ala	Gly	Lys	
			20					25					30			

gcc	tct	cgg	ctt	acc	ata	aac	gat	ctc	cac	aac	ttc	ctt	tcc	tat	ctc	144
Ala	Ser	Arg	Leu	Thr	Ile	Asn	Asp	Leu	His	Asn	Phe	Leu	Ser	Tyr	Leu	
			35				40					45				

caa	cac	aac	ctt	ata	aca	gta	act	tta	ctc	ttt	gct	ttc	act	ggt	ttc	192
Gln	His	Asn	Leu	Ile	Thr	Val	Thr	Leu	Leu	Phe	Ala	Phe	Thr	Val	Phe	
			50				55				60					

ggg	ttg	ggt	ctc	tac	atc	gta	acc	cga	ccc	aat	cgg	ggt	tat	ctc	ggt	240
Gly	Leu	Val	Leu	Tyr	Ile	Val	Thr	Arg	Pro	Asn	Pro	Val	Tyr	Leu	Val	
	65				70				75					80		

gac	tac	tcg	tgt	tac	ctt	cca	cca	cgg	cat	ctc	aaa	ggt	agt	gtc	tct	288
Asp	Tyr	Ser	Cys	Tyr	Leu	Pro	Pro	Pro	His	Leu	Lys	Val	Ser	Val	Ser	
				85					90					95		

aaa	gtc	atg	gat	att	ttc	tac	caa	ata	aga	aaa	gct	gat	act	tct	tca	336
Lys	Val	Met	Asp	Ile	Phe	Tyr	Gln	Ile	Arg	Lys	Ala	Asp	Thr	Ser	Ser	
			100				105					110				

cgg	aac	gtg	gca	tgt	gat	gat	cgg	tcc	tcg	ctc	gat	ttc	ctg	agg	aag	384
Arg	Asn	Val	Ala	Cys	Asp	Asp	Pro	Ser	Ser	Leu	Asp	Phe	Leu	Arg	Lys	
			115				120					125				

att	caa	gag	cgt	tca	ggg	cta	ggg	gat	gag	acg	tac	agt	cct	gag	gga	432
Ile	Gln	Glu	Arg	Ser	Gly	Leu	Gly	Asp	Glu	Thr	Tyr	Ser	Pro	Glu	Gly	

130				135				140									
ctc	att	cac	gta	cca	ccg	cgg	aag	act	ttt	gca	gcg	tca	cgt	gaa	gag	480	
Leu	Ile	His	Val	Pro	Pro	Arg	Lys	Thr	Phe	Ala	Ala	Ser	Arg	Glu	Glu		
145				150				155				160					
aca	gag	aag	gtt	atc	atc	ggt	gcg	ctc	gaa	aat	cta	ttc	gag	aac	acc	528	
Thr	Glu	Lys	Val	Ile	Ile	Gly	Ala	Leu	Glu	Asn	Leu	Phe	Glu	Asn	Thr		
				165				170				175					
aaa	gtt	aac	cct	aga	gag	att	ggt	ata	ctt	gtg	gtg	aac	tca	agc	atg	576	
Lys	Val	Asn	Pro	Arg	Glu	Ile	Gly	Ile	Leu	Val	Val	Asn	Ser	Ser	Met		
				180				185				190					
ttt	aat	cca	act	cct	tcg	cta	tcc	gct	atg	gtc	gtt	aat	act	ttc	aag	624	
Phe	Asn	Pro	Thr	Pro	Ser	Leu	Ser	Ala	Met	Val	Val	Asn	Thr	Phe	Lys		
				195				200				205					
ctc	cga	agc	aac	atc	aaa	agc	ttt	aat	cta	gga	gga	atg	ggt	tgt	agt	672	
Leu	Arg	Ser	Asn	Ile	Lys	Ser	Phe	Asn	Leu	Gly	Gly	Met	Gly	Cys	Ser		
				210				215				220					
gct	ggt	gtt	att	gcc	att	gat	ttg	gct	aaa	gac	ttg	ttg	cat	gtt	cat	720	
Ala	Gly	Val	Ile	Ala	Ile	Asp	Leu	Ala	Lys	Asp	Leu	Leu	His	Val	His		
				225				230				235				240	
aaa	aac	act	tat	gct	ctt	gtg	gtg	agc	act	gag	aac	atc	aca	caa	ggc	768	
Lys	Asn	Thr	Tyr	Ala	Leu	Val	Val	Ser	Thr	Glu	Asn	Ile	Thr	Gln	Gly		
				245				250				255					
att	tat	gct	gga	gaa	aat	aga	tca	atg	atg	gtt	agc	aat	tgc	ttg	ttt	816	
Ile	Tyr	Ala	Gly	Glu	Asn	Arg	Ser	Met	Met	Val	Ser	Asn	Cys	Leu	Phe		
				260				265				270					
cgt	gtt	ggt	ggg	gcc	gcg	att	ttg	ctc	tct	aac	aag	tcg	gga	gac	cgg	864	
Arg	Val	Gly	Gly	Ala	Ala	Ile	Leu	Leu	Ser	Asn	Lys	Ser	Gly	Asp	Arg		
				275				280				285					
aga	cgg	tcc	aag	tac	aag	cta	gtt	cac	acg	gtc	cga	acg	cat	act	gga	912	
Arg	Arg	Ser	Lys	Tyr	Lys	Leu	Val	His	Thr	Val	Arg	Thr	His	Thr	Gly		
				290				295				300					
gct	gat	gac	aag	tct	ttt	cga	tgt	gtg	caa	caa	gaa	gac	gat	gag	agc	960	
Ala	Asp	Asp	Lys	Ser	Phe	Arg	Cys	Val	Gln	Gln	Glu	Asp	Asp	Glu	Ser		
				305				310				315				320	
ggc	aaa	atc	gga	gtt	tgt	ctg	tca	aag	gac	ata	acc	aat	gtt	gcg	ggg	1008	
Gly	Lys	Ile	Gly	Val	Cys	Leu	Ser	Lys	Asp	Ile	Thr	Asn	Val	Ala	Gly		
				325				330				335					
aca	aca	ctt	acg	aaa	aat	ata	gca	aca	ttg	ggt	ccg	ttg	att	ctt	cct	1056	
Thr	Thr	Leu	Thr	Lys	Asn	Ile	Ala	Thr	Leu	Gly	Pro	Leu	Ile	Leu	Pro		
				340				345				350					
tta	agc	gaa	aag	ttt	ctt	ttt	ttc	gct	acc	ttc	gtc	gcc	aag	aaa	ctt	1104	
Leu	Ser	Glu	Lys	Phe	Leu	Phe	Phe	Ala	Thr	Phe	Val	Ala	Lys	Lys	Leu		
				355				360				365					

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   370                               375                               380

gtt gac cat ttc tgt att cat gcc gga ggc aga gcc gtg atc gat gtg      1200
Val Asp His Phe Cys Ile His Ala Gly Gly Arg Ala Val Ile Asp Val
   385                               390                               395                               400

cta gag aag aac cta gcc cta gca ccg atc gat gta gag gca tca aga      1248
Leu Glu Lys Asn Leu Ala Leu Ala Pro Ile Asp Val Glu Ala Ser Arg
                   405                               410                               415

tca acg tta cat aga ttt gga aac act tca tct agc tca ata tgg tat      1296
Ser Thr Leu His Arg Phe Gly Asn Thr Ser Ser Ser Ser Ile Trp Tyr
                   420                               425                               430

gag ttg gca tac ata gaa gca aaa gga agg atg aag aaa ggt aat aaa      1344
Glu Leu Ala Tyr Ile Glu Ala Lys Gly Arg Met Lys Lys Gly Asn Lys
   435                               440                               445

gtt tgg cag att gct tta ggg tca ggc ttt aag tgt aac agt gca gtt      1392
Val Trp Gln Ile Ala Leu Gly Ser Gly Phe Lys Cys Asn Ser Ala Val
   450                               455                               460

tgg gtg gct cta aac aat gtc aaa gct tcg aca aat agt cct tgg gaa      1440
Trp Val Ala Leu Asn Asn Val Lys Ala Ser Thr Asn Ser Pro Trp Glu
   465                               470                               475                               480

cac tgc atc gac aga tac ccg gtc aaa att gat tct gat tca ggt aag      1488
His Cys Ile Asp Arg Tyr Pro Val Lys Ile Asp Ser Asp Ser Gly Lys
                   485                               490                               495

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<210> 30
<211> 506
<212> PRT
<213> Artificial Sequence

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<223> Xaa = Pro or Gln

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      20           25           30

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35 40 45
Gln His Asn Leu Ile Thr Val Thr Leu Leu Phe Ala Phe Thr Val Phe
50 55 60
Gly Leu Val Leu Tyr Ile Val Thr Arg Pro Asn Pro Val Tyr Leu Val
65 70 75 80
Asp Tyr Ser Cys Tyr Leu Pro Pro Pro His Leu Lys Val Ser Val Ser
85 90 95
Lys Val Met Asp Ile Phe Tyr Gln Ile Arg Lys Ala Asp Thr Ser Ser
100 105 110
Arg Asn Val Ala Cys Asp Asp Pro Ser Ser Leu Asp Phe Leu Arg Lys
115 120 125
Ile Gln Glu Arg Ser Gly Leu Gly Asp Glu Thr Tyr Ser Pro Glu Gly
130 135 140
Leu Ile His Val Pro Pro Arg Lys Thr Phe Ala Ala Ser Arg Glu Glu
145 150 155 160
Thr Glu Lys Val Ile Ile Gly Ala Leu Glu Asn Leu Phe Glu Asn Thr
165 170 175
Lys Val Asn Pro Arg Glu Ile Gly Ile Leu Val Val Asn Ser Ser Met
180 185 190
Phe Asn Pro Thr Pro Ser Leu Ser Ala Met Val Val Asn Thr Phe Lys
195 200 205
Leu Arg Ser Asn Ile Lys Ser Phe Asn Leu Gly Gly Met Gly Cys Ser
210 215 220
Ala Gly Val Ile Ala Ile Asp Leu Ala Lys Asp Leu Leu His Val His
225 230 235 240
Lys Asn Thr Tyr Ala Leu Val Val Ser Thr Glu Asn Ile Thr Gln Gly
245 250 255
Ile Tyr Ala Gly Glu Asn Arg Ser Met Met Val Ser Asn Cys Leu Phe
260 265 270
Arg Val Gly Gly Ala Ala Ile Leu Leu Ser Asn Lys Ser Gly Asp Arg
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Ala Asp Asp Lys Ser Phe Arg Cys Val Gln Gln Glu Asp Asp Glu Ser
305 310 315 320
Gly Lys Ile Gly Val Cys Leu Ser Lys Asp Ile Thr Asn Val Ala Gly
325 330 335
Thr Thr Leu Thr Lys Asn Ile Ala Thr Leu Gly Pro Leu Ile Leu Pro
340 345 350
Leu Ser Glu Lys Phe Leu Phe Phe Ala Thr Phe Val Ala Lys Lys Leu
355 360 365
Leu Lys Asp Lys Ile Lys His Tyr Tyr Val Pro Asp Phe Lys Leu Ala
370 375 380
Val Asp His Phe Cys Ile His Ala Gly Gly Arg Ala Val Ile Asp Val
385 390 395 400
Leu Glu Lys Asn Leu Ala Leu Ala Pro Ile Asp Val Glu Ala Ser Arg
405 410 415
Ser Thr Leu His Arg Phe Gly Asn Thr Ser Ser Ser Ser Ile Trp Tyr
420 425 430
Glu Leu Ala Tyr Ile Glu Ala Lys Gly Arg Met Lys Lys Gly Asn Lys
435 440 445
Val Trp Gln Ile Ala Leu Gly Ser Gly Phe Lys Cys Asn Ser Ala Val
450 455 460
Trp Val Ala Leu Asn Asn Val Lys Ala Ser Thr Asn Ser Pro Trp Glu
465 470 475 480
His Cys Ile Asp Arg Tyr Pro Val Lys Ile Asp Ser Asp Ser Gly Lys

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<210> 31
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 <213> Artificial Sequence

<220>
 <223> 5' 1197 bp from B. napus elongase KCS (SEQ ID
 NO:3) and 3' 324 bp from A. thaliana FAE1 (SEQ ID
 NO:1); designated Bn399

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 ctt ttc aac ctt tgc ttc ttt ccg tta acg gcg atc gtc gcc gga aaa 96
 Leu Phe Asn Leu Cys Phe Phe Pro Leu Thr Ala Ile Val Ala Gly Lys
 20 25 30
 gcc tat cgg ctt acc ata gac gat ctt cac cac tta tac tat tcc tat 144
 Ala Tyr Arg Leu Thr Ile Asp Asp Leu His His Leu Tyr Tyr Ser Tyr
 35 40 45
 ctc caa cac aac ctc ata acc atc gct cca ctc ttt gcc ttc acc gtt 192
 Leu Gln His Asn Leu Ile Thr Ile Ala Pro Leu Phe Ala Phe Thr Val
 50 55 60
 ttc ggt tcg gtt ctc tac atc gca acc cgg ccc aaa ccg gtt tac ctc 240
 Phe Gly Ser Val Leu Tyr Ile Ala Thr Arg Pro Lys Pro Val Tyr Leu
 65 70 75 80
 gtt gag tac tca tgc tac ctt cca cca acg cat tgt aga tca agt atc 288
 Val Glu Tyr Ser Cys Tyr Leu Pro Pro Thr His Cys Arg Ser Ser Ile
 85 90 95
 tcc aag gtc atg gat atc ttt tat caa gta aga aaa gct gat cct tct 336
 Ser Lys Val Met Asp Ile Phe Tyr Gln Val Arg Lys Ala Asp Pro Ser
 100 105 110
 cgg aac ggc acg tgc gat gac tcg tcg tgg ctt gac ttc ttg agg aag 384
 Arg Asn Gly Thr Cys Asp Asp Ser Ser Trp Leu Asp Phe Leu Arg Lys
 115 120 125
 att caa gaa cgt tca ggt cta ggc gat gaa act cac ggg ccc gag ggg 432
 Ile Gln Glu Arg Ser Gly Leu Gly Asp Glu Thr His Gly Pro Glu Gly
 130 135 140
 ctg ctt cag gtc cct ccc cgg aag act ttt gcg gcg gcg cgt gaa gag 480
 Leu Leu Gln Val Pro Pro Arg Lys Thr Phe Ala Ala Ala Arg Glu Glu
 145 150 155 160

acg gag caa gtt atc att ggt gcg cta gaa aat cta ttc aag aac acc	528
Thr Glu Gln Val Ile Ile Gly Ala Leu Glu Asn Leu Phe Lys Asn Thr	
165 170 175	
aac gtt aac cct aaa gat ata ggt ata ctt gtg gtg aac tca agc atg	576
Asn Val Asn Pro Lys Asp Ile Gly Ile Leu Val Val Asn Ser Ser Met	
180 185 190	
ttt aat cca act cca tcg ctc tcc gcg atg gtc gtt aac act ttc aag	624
Phe Asn Pro Thr Pro Ser Leu Ser Ala Met Val Val Asn Thr Phe Lys	
195 200 205	
ctc cga agc aac gta aga agc ttt aac ctt ggt ggc atg ggt tgt agt	672
Leu Arg Ser Asn Val Arg Ser Phe Asn Leu Gly Gly Met Gly Cys Ser	
210 215 220	
gcc ggc gtt ata gcc att gat cta gca aag gac ttg ttg cat gtc cat	720
Ala Gly Val Ile Ala Ile Asp Leu Ala Lys Asp Leu Leu His Val His	
225 230 235 240	
aaa aat acg tat gct ctt gtg gtg agc aca gag aac atc act tat aac	768
Lys Asn Thr Tyr Ala Leu Val Val Ser Thr Glu Asn Ile Thr Tyr Asn	
245 250 255	
att tac gct ggt gat aat agg tcc atg atg gtt tca aat tgc ttg ttc	816
Ile Tyr Ala Gly Asp Asn Arg Ser Met Met Val Ser Asn Cys Leu Phe	
260 265 270	
cgt gtt ggt ggg gcc gct att ttg ctc tcc aac aag cct gga gat cgt	864
Arg Val Gly Gly Ala Ala Ile Leu Leu Ser Asn Lys Pro Gly Asp Arg	
275 280 285	
aga cgg tcc aag tac gag cta gtt cac acg gtt cga acg cat acc gga	912
Arg Arg Ser Lys Tyr Glu Leu Val His Thr Val Arg Thr His Thr Gly	
290 295 300	
gct gac ggc aag tct ttt cgt tgc gtg caa caa gga gac gat gag aac	960
Ala Asp Gly Lys Ser Phe Arg Cys Val Gln Gln Gly Asp Asp Glu Asn	
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Gly Lys Ile Gly Val Ser Leu Ser Lys Asp Ile Thr Asp Val Ala Gly	
325 330 335	
cga acg gtt aag aaa aac ata gca acg ttg ggt ccg ttg att ctt ccg	1056
Arg Thr Val Lys Lys Asn Ile Ala Thr Leu Gly Pro Leu Ile Leu Pro	
340 345 350	
tta agc gag aaa ctt ctt ttt ttc gtt acc ttc atg ggc aag aaa ctt	1104
Leu Ser Glu Lys Leu Leu Phe Phe Val Thr Phe Met Gly Lys Lys Leu	
355 360 365	
ttc aaa gat aaa atc aaa cat tac tac gtc ccg gat ttc aaa ctt gct	1152
Phe Lys Asp Lys Ile Lys His Tyr Tyr Val Pro Asp Phe Lys Leu Ala	
370 375 380	

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cat tgc atc gat aga tat ccg gtt aaa att gat tct gat ttg tca aag 1488
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<213> Artificial Sequence

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 FAE1 (SEQ ID NO:1); designated Bn399

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Ile	Tyr	Ala	Gly	Asp	Asn	Arg	Ser	Met	Met	Val	Ser	Asn	Cys	Leu	Phe		
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Arg	Thr	Val	Lys	Lys	Asn	Ile	Ala	Thr	Leu	Gly	Pro	Leu	Ile	Leu	Pro		
			340					345				350					
Leu	Ser	Glu	Lys	Leu	Leu	Phe	Phe	Val	Thr	Phe	Met	Gly	Lys	Lys	Leu		
		355				360					365						
Phe	Lys	Asp	Lys	Ile	Lys	His	Tyr	Tyr	Val	Pro	Asp	Phe	Lys	Leu	Ala		
		370				375					380						
Ile	Asp	His	Phe	Cys	Ile	His	Ala	Gly	Gly	Arg	Ala	Val	Ile	Asp	Glu		
385					390					395					400		
Leu	Glu	Lys	Asn	Leu	Gly	Leu	Ser	Pro	Ile	Asp	Val	Glu	Ala	Ser	Arg		
				405					410					415			
Ser	Thr	Leu	His	Arg	Phe	Gly	Asn	Thr	Ser	Ser	Ser	Ser	Ile	Trp	Tyr		
			420					425					430				
Glu	Leu	Ala	Tyr	Ile	Glu	Ala	Lys	Gly	Arg	Met	Lys	Lys	Gly	Asn	Lys		
		435					440					445					
Ala	Trp	Gln	Ile	Ala	Leu	Gly	Ser	Gly	Phe	Lys	Cys	Asn	Ser	Ala	Val		
		450				455					460						
Trp	Val	Ala	Leu	Arg	Asn	Val	Lys	Ala	Ser	Ala	Asn	Ser	Pro	Trp	Gln		
465					470					475					480		
His	Cys	Ile	Asp	Arg	Tyr	Pro	Val	Lys	Ile	Asp	Ser	Asp	Leu	Ser	Lys		
				485					490					495			
Ser	Lys	Thr	His	Val	Gln	Asn	Gly	Arg	Ser								
			500					505									

<210> 33

<211> 1524

<212> DNA

<213> Artificial Sequence

<220>

<223> 1524 bp from B. napus elongase KCS (SEQ ID NO:3)
having a mutation at position 920; designated Bn
G307D; hypothetical

<221> CDS

<222> (1)...(1518)

<400> 33

atg	acg	tcc	att	aac	gta	aag	ctc	ctt	tac	cat	tac	gtc	ata	acc	aac	48
Met	Thr	Ser	Ile	Asn	Val	Lys	Leu	Leu	Tyr	His	Tyr	Val	Ile	Thr	Asn	
1				5					10					15		

ctt	ttc	aac	ctt	tgc	ttc	ttt	ccg	tta	acg	gcg	atc	gtc	gcc	gga	aaa	96
Leu	Phe	Asn	Leu	Cys	Phe	Phe	Pro	Leu	Thr	Ala	Ile	Val	Ala	Gly	Lys	
			20					25					30			

gcc	tat	cgg	ctt	acc	ata	gac	gat	ctt	cac	cac	tta	tac	tat	tcc	tat	144
Ala	Tyr	Arg	Leu	Thr	Ile	Asp	Asp	Leu	His	His	Leu	Tyr	Tyr	Ser	Tyr	
		35					40					45				

ctc	caa	cac	aac	ctc	ata	acc	atc	gct	cca	ctc	ttt	gcc	ttc	acc	gtt	192
Leu	Gln	His	Asn	Leu	Ile	Thr	Ile	Ala	Pro	Leu	Phe	Ala	Phe	Thr	Val	
	50					55					60					

ttc	ggg	tcg	gtt	ctc	tac	atc	gca	acc	cgg	ccc	aaa	ccg	gtt	tac	ctc	240
Phe	Gly	Ser	Val	Leu	Tyr	Ile	Ala	Thr	Arg	Pro	Lys	Pro	Val	Tyr	Leu	
65					70					75					80	

gtt	gag	tac	tca	tgc	tac	ctt	cca	cca	acg	cat	tgt	aga	tca	agt	atc	288
Val	Glu	Tyr	Ser	Cys	Tyr	Leu	Pro	Pro	Thr	His	Cys	Arg	Ser	Ser	Ile	
				85					90					95		

tcc	aag	gtc	atg	gat	atc	ttt	tat	caa	gta	aga	aaa	gct	gat	cct	tct	336
Ser	Lys	Val	Met	Asp	Ile	Phe	Tyr	Gln	Val	Arg	Lys	Ala	Asp	Pro	Ser	
			100					105					110			

cgg	aac	ggc	acg	tgc	gat	gac	tcg	tcg	tgg	ctt	gac	ttc	ttg	agg	aag	384
Arg	Asn	Gly	Thr	Cys	Asp	Asp	Ser	Ser	Trp	Leu	Asp	Phe	Leu	Arg	Lys	
		115					120					125				

att	caa	gaa	cgt	tca	ggg	cta	ggc	gat	gaa	act	cac	ggg	ccc	gag	ggg	432
Ile	Gln	Glu	Arg	Ser	Gly	Leu	Gly	Asp	Glu	Thr	His	Gly	Pro	Glu	Gly	
	130					135					140					

ctg	ctt	cag	gtc	cct	ccc	cgg	aag	act	ttt	gcg	gcg	gcg	cgt	gaa	gag	480
Leu	Leu	Gln	Val	Pro	Pro	Arg	Lys	Thr	Phe	Ala	Ala	Ala	Arg	Glu	Glu	
145					150					155					160	

acg	gag	caa	gtt	atc	att	ggg	gcg	cta	gaa	aat	cta	ttc	aag	aac	acc	528
Thr	Glu	Gln	Val	Ile	Ile	Gly	Ala	Leu	Glu	Asn	Leu	Phe	Lys	Asn	Thr	
				165					170					175		

aac	gtt	aac	cct	aaa	gat	ata	ggg	ata	ctt	gtg	gtg	aac	tca	agc	atg	576
Asn	Val	Asn	Pro	Lys	Asp	Ile	Gly	Ile	Leu	Val	Val	Asn	Ser	Ser	Met	
			180					185						190		

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ttt aat cca act cca tcg ctc tcc gcg atg gtc gtt aac act ttc aag	624
Phe Asn Pro Thr Pro Ser Leu Ser Ala Met Val Val Asn Thr Phe Lys	
195 200 205	
ctc cga agc aac gta aga agc ttt aac ctt ggt ggc atg ggt tgt agt	672
Leu Arg Ser Asn Val Arg Ser Phe Asn Leu Gly Gly Met Gly Cys Ser	
210 215 220	
gcc ggc gtt ata gcc att gat cta gca aag gac ttg ttg cat gtc cat	720
Ala Gly Val Ile Ala Ile Asp Leu Ala Lys Asp Leu Leu His Val His	
225 230 235 240	
aaa aat acg tat gct ctt gtg gtg agc aca gag aac atc act tat aac	768
Lys Asn Thr Tyr Ala Leu Val Val Ser Thr Glu Asn Ile Thr Tyr Asn	
245 250 255	
att tac gct ggt gat aat agg tcc atg atg gtt tca aat tgc ttg ttc	816
Ile Tyr Ala Gly Asp Asn Arg Ser Met Met Val Ser Asn Cys Leu Phe	
260 265 270	
cgt gtt ggt ggg gcc gct att ttg ctc tcc aac aag cct gga gat cgt	864
Arg Val Gly Gly Ala Ala Ile Leu Leu Ser Asn Lys Pro Gly Asp Arg	
275 280 285	
aga cgg tcc aag tac gag cta gtt cac acg gtt cga acg cat acc gga	912
Arg Arg Ser Lys Tyr Glu Leu Val His Thr Val Arg Thr His Thr Gly	
290 295 300	
gct gac gac aag tct ttt cgt tgc gtg caa caa gga gac gat gag aac	960
Ala Asp Asp Lys Ser Phe Arg Cys Val Gln Gln Gly Asp Asp Glu Asn	
305 310 315 320	
ggc aaa atc gga gtg agt ttg tcc aag gac ata acc gat gtt gct ggt	1008
Gly Lys Ile Gly Val Ser Leu Ser Lys Asp Ile Thr Asp Val Ala Gly	
325 330 335	
cga acg gtt aag aaa aac ata gca acg ttg ggt ccg ttg att ctt ccg	1056
Arg Thr Val Lys Lys Asn Ile Ala Thr Leu Gly Pro Leu Ile Leu Pro	
340 345 350	
tta agc gag aaa ctt ctt ttt ttc gtt acc ttc atg ggc aag aaa ctt	1104
Leu Ser Glu Lys Leu Leu Phe Phe Val Thr Phe Met Gly Lys Lys Leu	
355 360 365	
ttc aaa gat aaa atc aaa cat tac tac gtc ccg gat ttc aaa ctt gct	1152
Phe Lys Asp Lys Ile Lys His Tyr Tyr Val Pro Asp Phe Lys Leu Ala	
370 375 380	
att gac cat ttt tgt ata cat gcc gga ggc aga gcc gtg att gat gtg	1200
Ile Asp His Phe Cys Ile His Ala Gly Gly Arg Ala Val Ile Asp Val	
385 390 395 400	
cta gag aag aac cta gcc cta gca ccg atc gat gta gag gca tca aga	1248
Leu Glu Lys Asn Leu Ala Leu Ala Pro Ile Asp Val Glu Ala Ser Arg	
405 410 415	
tca acg tta cat aga ttt gga aac act tca tct agc tca ata tgg tat	1296

Ser Thr Leu His Arg Phe Gly Asn Thr Ser Ser Ser Ser Ile Trp Tyr
420 425 430

gag ttg gca tac ata gaa gca aaa gga agg atg aag aaa ggt aat aaa 1344
Glu Leu Ala Tyr Ile Glu Ala Lys Gly Arg Met Lys Lys Gly Asn Lys
435 440 445

gtt tgg cag att gct tta ggg tca ggc ttt aag tgt aac agt gca gtt 1392
Val Trp Gln Ile Ala Leu Gly Ser Gly Phe Lys Cys Asn Ser Ala Val
450 455 460

tgg gtg gct cta aac aat gtc aaa gct tcg aca aat agt cct tgg gaa 1440
Trp Val Ala Leu Asn Asn Val Lys Ala Ser Thr Asn Ser Pro Trp Glu
465 470 475 480

cac tgc atc gac aga tac ccg gtc aaa att gat tct gat tca ggt aag 1488
His Cys Ile Asp Arg Tyr Pro Val Lys Ile Asp Ser Asp Ser Gly Lys
485 490 495

tca gag act cgt gtc caa aac ggt cgg tcc taataa 1524
Ser Glu Thr Arg Val Gln Asn Gly Arg Ser
500 505

<210> 34
<211> 506
<212> PRT
<213> Artificial Sequence

<220>
<223> 506 amino acids from B. napus elongase KCS (SEQ ID
NO:4) having a mutation at residue 307; designated
Bn G307D; hypothetical

<400> 34
Met Thr Ser Ile Asn Val Lys Leu Leu Tyr His Tyr Val Ile Thr Asn
1 5 10 15
Leu Phe Asn Leu Cys Phe Phe Pro Leu Thr Ala Ile Val Ala Gly Lys
20 25 30
Ala Tyr Arg Leu Thr Ile Asp Asp Leu His His Leu Tyr Tyr Ser Tyr
35 40 45
Leu Gln His Asn Leu Ile Thr Ile Ala Pro Leu Phe Ala Phe Thr Val
50 55 60
Phe Gly Ser Val Leu Tyr Ile Ala Thr Arg Pro Lys Pro Val Tyr Leu
65 70 75 80
Val Glu Tyr Ser Cys Tyr Leu Pro Pro Thr His Cys Arg Ser Ser Ile
85 90 95
Ser Lys Val Met Asp Ile Phe Tyr Gln Val Arg Lys Ala Asp Pro Ser
100 105 110
Arg Asn Gly Thr Cys Asp Asp Ser Ser Trp Leu Asp Phe Leu Arg Lys
115 120 125
Ile Gln Glu Arg Ser Gly Leu Gly Asp Glu Thr His Gly Pro Glu Gly
130 135 140
Leu Leu Gln Val Pro Pro Arg Lys Thr Phe Ala Ala Arg Glu Glu
145 150 155 160
Thr Glu Gln Val Ile Ile Gly Ala Leu Glu Asn Leu Phe Lys Asn Thr
165 170 175

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Asn Val Asn Pro Lys Asp Ile Gly Ile Leu Val Val Asn Ser Ser Met
      180      185      190
Phe Asn Pro Thr Pro Ser Leu Ser Ala Met Val Val Asn Thr Phe Lys
      195      200      205
Leu Arg Ser Asn Val Arg Ser Phe Asn Leu Gly Gly Met Gly Cys Ser
      210      215      220
Ala Gly Val Ile Ala Ile Asp Leu Ala Lys Asp Leu Leu His Val His
      225      230      235      240
Lys Asn Thr Tyr Ala Leu Val Val Ser Thr Glu Asn Ile Thr Tyr Asn
      245      250      255
Ile Tyr Ala Gly Asp Asn Arg Ser Met Met Val Ser Asn Cys Leu Phe
      260      265      270
Arg Val Gly Gly Ala Ala Ile Leu Leu Ser Asn Lys Pro Gly Asp Arg
      275      280      285
Arg Arg Ser Lys Tyr Glu Leu Val His Thr Val Arg Thr His Thr Gly
      290      295      300
Ala Asp Asp Lys Ser Phe Arg Cys Val Gln Gln Gly Asp Asp Glu Asn
      305      310      315      320
Gly Lys Ile Gly Val Ser Leu Ser Lys Asp Ile Thr Asp Val Ala Gly
      325      330      335
Arg Thr Val Lys Lys Asn Ile Ala Thr Leu Gly Pro Leu Ile Leu Pro
      340      345      350
Leu Ser Glu Lys Leu Leu Phe Phe Val Thr Phe Met Gly Lys Lys Leu
      355      360      365
Phe Lys Asp Lys Ile Lys His Tyr Tyr Val Pro Asp Phe Lys Leu Ala
      370      375      380
Ile Asp His Phe Cys Ile His Ala Gly Gly Arg Ala Val Ile Asp Val
      385      390      395      400
Leu Glu Lys Asn Leu Ala Leu Ala Pro Ile Asp Val Glu Ala Ser Arg
      405      410      415
Ser Thr Leu His Arg Phe Gly Asn Thr Ser Ser Ser Ser Ile Trp Tyr
      420      425      430
Glu Leu Ala Tyr Ile Glu Ala Lys Gly Arg Met Lys Lys Gly Asn Lys
      435      440      445
Val Trp Gln Ile Ala Leu Gly Ser Gly Phe Lys Cys Asn Ser Ala Val
      450      455      460
Trp Val Ala Leu Asn Asn Val Lys Ala Ser Thr Asn Ser Pro Trp Glu
      465      470      475      480
His Cys Ile Asp Arg Tyr Pro Val Lys Ile Asp Ser Asp Ser Gly Lys
      485      490      495
Ser Glu Thr Arg Val Gln Asn Gly Arg Ser
      500      505

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<210> 35

<211> 1709

<212> DNA

<213> Artificial Sequence

<220>

<223> 1709 bp from A. thaliana FAEl (SEQ ID NO:1) having
a mutation at position 275; designated At K92R;
hypothetical

<221> CDS

<222> (1)...(1518)

<400> 35

atg acg tcc gtt aac gtt aag ctc ctt tac cgt tac gtc tta acc aac	48
Met Thr Ser Val Asn Val Lys Leu Leu Tyr Arg Tyr Val Leu Thr Asn	
1 5 10 15	
ttt ttc aac ctc tgt ttg ttc ccg tta acg gcg ttc ctc gcc gga aaa	96
Phe Phe Asn Leu Cys Leu Phe Pro Leu Thr Ala Phe Leu Ala Gly Lys	
20 25 30	
gcc tct cgg ctt acc ata aac gat ctc cac aac ttc ctt tcc tat ctc	144
Ala Ser Arg Leu Thr Ile Asn Asp Leu His Asn Phe Leu Ser Tyr Leu	
35 40 45	
caa cac aac ctt ata aca gta act tta ctc ttt gct ttc act gtt ttc	192
Gln His Asn Leu Ile Thr Val Thr Leu Leu Phe Ala Phe Thr Val Phe	
50 55 60	
ggg ttg gtt ctc tac atc gta acc cga ccc aat ccg gtt tat ctc gtt	240
Gly Leu Val Leu Tyr Ile Val Thr Arg Pro Asn Pro Val Tyr Leu Val	
65 70 75 80	
gac tac tcg tgt tac ctt cca cca ccg cat ctc aga gtt agt gtc tct	288
Asp Tyr Ser Cys Tyr Leu Pro Pro Pro His Leu Arg Val Ser Val Ser	
85 90 95	
aaa gtc atg gat att ttc tac caa ata aga aaa gct gat act tct tca	336
Lys Val Met Asp Ile Phe Tyr Gln Ile Arg Lys Ala Asp Thr Ser Ser	
100 105 110	
cgg aac gtg gca tgt gat gat ccg tcc tcg ctc gat ttc ctg agg aag	384
Arg Asn Val Ala Cys Asp Asp Pro Ser Ser Leu Asp Phe Leu Arg Lys	
115 120 125	
att caa gag cgt tca ggt cta ggt gat gag acg tac agt cct gag gga	432
Ile Gln Glu Arg Ser Gly Leu Gly Asp Glu Thr Tyr Ser Pro Glu Gly	
130 135 140	
ctc att cac gta cca ccg cgg aag act ttt gca gcg tca cgt gaa gag	480
Leu Ile His Val Pro Pro Arg Lys Thr Phe Ala Ala Ser Arg Glu Glu	
145 150 155 160	
aca gag aag gtt atc atc ggt gcg ctc gaa aat cta ttc gag aac acc	528
Thr Glu Lys Val Ile Ile Gly Ala Leu Glu Asn Leu Phe Glu Asn Thr	
165 170 175	
aaa gtt aac cct aga gag att ggt ata ctt gtg gtg aac tca agc atg	576
Lys Val Asn Pro Arg Glu Ile Gly Ile Leu Val Val Asn Ser Ser Met	
180 185 190	
ttt aat cca act cct tcg cta tcc gct atg gtc gtt aat act ttc aag	624
Phe Asn Pro Thr Pro Ser Leu Ser Ala Met Val Val Asn Thr Phe Lys	
195 200 205	
ctc cga agc aac atc aaa agc ttt aat cta gga gga atg ggt tgt agt	672
Leu Arg Ser Asn Ile Lys Ser Phe Asn Leu Gly Gly Met Gly Cys Ser	
210 215 220	
gct ggt gtt att gcc att gat ttg gct aaa gac ttg ttg cat gtt cat	720

Ala Gly Val Ile Ala Ile Asp Leu Ala Lys Asp Leu Leu His Val His	
225 230 235 240	
aaa aac act tat gct ctt gtg gtg agc act gag aac atc aca caa ggc	768
Lys Asn Thr Tyr Ala Leu Val Val Ser Thr Glu Asn Ile Thr Gln Gly	
245 250 255	
att tat gct gga gaa aat aga tca atg atg gtt agc aat tgc ttg ttt	816
Ile Tyr Ala Gly Glu Asn Arg Ser Met Met Val Ser Asn Cys Leu Phe	
260 265 270	
cgt gtt ggt ggg gcc gcg att ttg ctc tct aac aag tcg gga gac cgg	864
Arg Val Gly Gly Ala Ala Ile Leu Leu Ser Asn Lys Ser Gly Asp Arg	
275 280 285	
aga cgg tcc aag tac aag cta gtt cac acg gtc cga acg cat act gga	912
Arg Arg Ser Lys Tyr Lys Leu Val His Thr Val Arg Thr His Thr Gly	
290 295 300	
gct gat gac aag tct ttt cga tgt gtg caa caa gaa gac gat gag agc	960
Ala Asp Asp Lys Ser Phe Arg Cys Val Gln Gln Glu Asp Asp Glu Ser	
305 310 315 320	
ggc aaa atc gga gtt tgt ctg tca aag gac ata acc aat gtt gcg ggg	1008
Gly Lys Ile Gly Val Cys Leu Ser Lys Asp Ile Thr Asn Val Ala Gly	
325 330 335	
aca aca ctt acg aaa aat ata gca aca ttg ggt ccg ttg att ctt cct	1056
Thr Thr Leu Thr Lys Asn Ile Ala Thr Leu Gly Pro Leu Ile Leu Pro	
340 345 350	
tta agc gaa aag ttt ctt ttt ttc gct acc ttc gtc gcc aag aaa ctt	1104
Leu Ser Glu Lys Phe Leu Phe Phe Ala Thr Phe Val Ala Lys Lys Leu	
355 360 365	
cta aag gat aaa atc aag cat tac tat gtt ccg gat ttc aag ctt gct	1152
Leu Lys Asp Lys Ile Lys His Tyr Tyr Val Pro Asp Phe Lys Leu Ala	
370 375 380	
gtt gac cat ttc tgt att cat gcc gga ggc aga gcc gtg atc gat gag	1200
Val Asp His Phe Cys Ile His Ala Gly Gly Arg Ala Val Ile Asp Glu	
385 390 395 400	
cta gag aag aac tta gga cta tcg ccg atc gat gtg gag gca tct aga	1248
Leu Glu Lys Asn Leu Gly Leu Ser Pro Ile Asp Val Glu Ala Ser Arg	
405 410 415	
tca acg tta cat aga ttt ggg aat act tca tct agc tca att tgg tat	1296
Ser Thr Leu His Arg Phe Gly Asn Thr Ser Ser Ser Ser Ile Trp Tyr	
420 425 430	
gaa tta gca tac ata gag gca aag gga aga atg aag aaa ggg aat aaa	1344
Glu Leu Ala Tyr Ile Glu Ala Lys Gly Arg Met Lys Lys Gly Asn Lys	
435 440 445	
gct tgg cag att gct tta gga tca ggg ttt aag tgt aat agt gcg gtt	1392
Ala Trp Gln Ile Ala Leu Gly Ser Gly Phe Lys Cys Asn Ser Ala Val	

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450                               455                               460
tgg gtg gct cta cgc aat gtc aag gca tcg gca aat agt cct tgg caa      1440
Trp Val Ala Leu Arg Asn Val Lys Ala Ser Ala Asn Ser Pro Trp Gln
465                               470                               475                               480

cat tgc atc gat aga tat ccg gtt aaa att gat tct gat ttg tca aag      1488
His Cys Ile Asp Arg Tyr Pro Val Lys Ile Asp Ser Asp Leu Ser Lys
485                               490                               495

tca aag act cat gtc caa aac ggt cgg tcc taatttgatg tatctgagtg      1538
Ser Lys Thr His Val Gln Asn Gly Arg Ser
500                               505

ccaacggttta ctttgtcttt cctttctttt attgggttatg aattagatgt ttactaatgt      1598
tcctctcttt ttcggtataa ataaagaagt tcaattcttc ctatagtttc aaacgcgatt      1658
ttaagcggtt ctatttaggt ttacatgaat ttcttttaca aaccatcttt t      1709

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<210> 36

<211> 506

<212> PRT

<213> Artificial Sequence

<220>

<223> 506 amino acids from A. thaliana FAE1 (SEQ ID
NO:2) having a mutation at residue 92; designated
At K92R; hypothetical

<400> 36

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Met Thr Ser Val Asn Val Lys Leu Leu Tyr Arg Tyr Val Leu Thr Asn
1           5           10           15
Phe Phe Asn Leu Cys Leu Phe Pro Leu Thr Ala Phe Leu Ala Gly Lys
20           25           30
Ala Ser Arg Leu Thr Ile Asn Asp Leu His Asn Phe Leu Ser Tyr Leu
35           40           45
Gln His Asn Leu Ile Thr Val Thr Leu Leu Phe Ala Phe Thr Val Phe
50           55           60
Gly Leu Val Leu Tyr Ile Val Thr Arg Pro Asn Pro Val Tyr Leu Val
65           70           75           80
Asp Tyr Ser Cys Tyr Leu Pro Pro Pro His Leu Arg Val Ser Val Ser
85           90           95
Lys Val Met Asp Ile Phe Tyr Gln Ile Arg Lys Ala Asp Thr Ser Ser
100          105          110
Arg Asn Val Ala Cys Asp Asp Pro Ser Ser Leu Asp Phe Leu Arg Lys
115          120          125
Ile Gln Glu Arg Ser Gly Leu Gly Asp Glu Thr Tyr Ser Pro Glu Gly
130          135          140
Leu Ile His Val Pro Pro Arg Lys Thr Phe Ala Ala Ser Arg Glu Glu
145          150          155          160
Thr Glu Lys Val Ile Ile Gly Ala Leu Glu Asn Leu Phe Glu Asn Thr
165          170          175
Lys Val Asn Pro Arg Glu Ile Gly Ile Leu Val Val Asn Ser Ser Met
180          185          190
Phe Asn Pro Thr Pro Ser Leu Ser Ala Met Val Val Asn Thr Phe Lys
195          200          205
Leu Arg Ser Asn Ile Lys Ser Phe Asn Leu Gly Gly Met Gly Cys Ser
210          215          220

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Ala Gly Val Ile Ala Ile Asp Leu Ala Lys Asp Leu Leu His Val His
 225 230 235 240
 Lys Asn Thr Tyr Ala Leu Val Val Ser Thr Glu Asn Ile Thr Gln Gly
 245 250 255
 Ile Tyr Ala Gly Glu Asn Arg Ser Met Met Val Ser Asn Cys Leu Phe
 260 265 270
 Arg Val Gly Gly Ala Ala Ile Leu Leu Ser Asn Lys Ser Gly Asp Arg
 275 280 285
 Arg Arg Ser Lys Tyr Lys Leu Val His Thr Val Arg Thr His Thr Gly
 290 295 300
 Ala Asp Asp Lys Ser Phe Arg Cys Val Gln Gln Glu Asp Asp Glu Ser
 305 310 315 320
 Gly Lys Ile Gly Val Cys Leu Ser Lys Asp Ile Thr Asn Val Ala Gly
 325 330 335
 Thr Thr Leu Thr Lys Asn Ile Ala Thr Leu Gly Pro Leu Ile Leu Pro
 340 345 350
 Leu Ser Glu Lys Phe Leu Phe Phe Ala Thr Phe Val Ala Lys Lys Leu
 355 360 365
 Leu Lys Asp Lys Ile Lys His Tyr Tyr Val Pro Asp Phe Lys Leu Ala
 370 375 380
 Val Asp His Phe Cys Ile His Ala Gly Gly Arg Ala Val Ile Asp Glu
 385 390 395 400
 Leu Glu Lys Asn Leu Gly Leu Ser Pro Ile Asp Val Glu Ala Ser Arg
 405 410 415
 Ser Thr Leu His Arg Phe Gly Asn Thr Ser Ser Ser Ser Ile Trp Tyr
 420 425 430
 Glu Leu Ala Tyr Ile Glu Ala Lys Gly Arg Met Lys Lys Gly Asn Lys
 435 440 445
 Ala Trp Gln Ile Ala Leu Gly Ser Gly Phe Lys Cys Asn Ser Ala Val
 450 455 460
 Trp Val Ala Leu Arg Asn Val Lys Ala Ser Ala Asn Ser Pro Trp Gln
 465 470 475 480
 His Cys Ile Asp Arg Tyr Pro Val Lys Ile Asp Ser Asp Leu Ser Lys
 485 490 495
 Ser Lys Thr His Val Gln Asn Gly Arg Ser
 500 505

<210> 37
 <211> 1521
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> 5' 762 bp from A. thaliana FAE1 (SEQ ID NO:1) and
 3' 759 bp from B. napus elongase KCS (SEQ ID NO:3)
 and having a mutation at position 920; designated
 At254 G307D; hypothetical

<221> CDS
 <222> (1)...(1518)

<400> 37
 atg acg tcc gtt aac gtt aag ctc ctt tac cgt tac gtc tta acc aac
 Met Thr Ser Val Asn Val Lys Leu Leu Tyr Arg Tyr Val Leu Thr Asn
 1 5 10 15

48

ttt ttc aac ctc tgt ttg ttc ccg tta acg gcg ttc ctc gcc gga aaa

96

Phe	Phe	Asn	Leu	Cys	Leu	Phe	Pro	Leu	Thr	Ala	Phe	Leu	Ala	Gly	Lys	
		20						25					30			
gcc	tct	cgg	ctt	acc	ata	aac	gat	ctc	cac	aac	ttc	ctt	tcc	tat	ctc	144
Ala	Ser	Arg	Leu	Thr	Ile	Asn	Asp	Leu	His	Asn	Phe	Leu	Ser	Tyr	Leu	
		35					40					45				
caa	cac	aac	ctt	ata	aca	gta	act	tta	ctc	ttt	gct	ttc	act	gtt	ttc	192
Gln	His	Asn	Leu	Ile	Thr	Val	Thr	Leu	Leu	Phe	Ala	Phe	Thr	Val	Phe	
	50					55				60						
ggg	ttg	gtt	ctc	tac	atc	gta	acc	cga	ccc	aat	ccg	gtt	tat	ctc	gtt	240
Gly	Leu	Val	Leu	Tyr	Ile	Val	Thr	Arg	Pro	Asn	Pro	Val	Tyr	Leu	Val	
	65				70				75					80		
gac	tac	tcg	tgt	tac	ctt	cca	cca	ccg	cat	ctc	aaa	gtt	agt	gtc	tct	288
Asp	Tyr	Ser	Cys	Tyr	Leu	Pro	Pro	Pro	His	Leu	Lys	Val	Ser	Val	Ser	
			85						90				95			
aaa	gtc	atg	gat	att	ttc	tac	caa	ata	aga	aaa	gct	gat	act	tct	tca	336
Lys	Val	Met	Asp	Ile	Phe	Tyr	Gln	Ile	Arg	Lys	Ala	Asp	Thr	Ser	Ser	
		100					105					110				
cgg	aac	gtg	gca	tgt	gat	gat	ccg	tcc	tcg	ctc	gat	ttc	ctg	agg	aag	384
Arg	Asn	Val	Ala	Cys	Asp	Asp	Pro	Ser	Ser	Leu	Asp	Phe	Leu	Arg	Lys	
		115					120					125				
att	caa	gag	cgt	tca	ggg	cta	ggg	gat	gag	acg	tac	agt	cct	gag	gga	432
Ile	Gln	Glu	Arg	Ser	Gly	Leu	Gly	Asp	Glu	Thr	Tyr	Ser	Pro	Glu	Gly	
	130					135					140					
ctc	att	cac	gta	cca	ccg	cgg	aag	act	ttt	gca	gcg	tca	cgt	gaa	gag	480
Leu	Ile	His	Val	Pro	Pro	Arg	Lys	Thr	Phe	Ala	Ala	Ser	Arg	Glu	Glu	
	145				150					155				160		
aca	gag	aag	gtt	atc	atc	ggg	gcg	ctc	gaa	aat	cta	ttc	gag	aac	acc	528
Thr	Glu	Lys	Val	Ile	Ile	Gly	Ala	Leu	Glu	Asn	Leu	Phe	Glu	Asn	Thr	
			165					170					175			
aaa	gtt	aac	cct	aga	gag	att	ggg	ata	ctt	gtg	gtg	aac	tca	agc	atg	576
Lys	Val	Asn	Pro	Arg	Glu	Ile	Gly	Ile	Leu	Val	Val	Asn	Ser	Ser	Met	
		180					185					190				
ttt	aat	cca	act	cct	tcg	cta	tcc	gct	atg	gtc	gtt	aat	act	ttc	aag	624
Phe	Asn	Pro	Thr	Pro	Ser	Leu	Ser	Ala	Met	Val	Val	Asn	Thr	Phe	Lys	
		195					200					205				
ctc	cga	agc	aac	atc	aaa	agc	ttt	aat	cta	gga	gga	atg	ggg	tgt	agt	672
Leu	Arg	Ser	Asn	Ile	Lys	Ser	Phe	Asn	Leu	Gly	Gly	Met	Gly	Cys	Ser	
	210					215					220					
gct	ggg	gtt	att	gcc	att	gat	ttg	gct	aaa	gac	ttg	ttg	cat	gtt	cat	720
Ala	Gly	Val	Ile	Ala	Ile	Asp	Leu	Ala	Lys	Asp	Leu	Leu	His	Val	His	
	225				230				235					240		
aaa	aac	act	tat	gct	ctc	gtg	gtg	agc	aca	gag	aac	atc	act	tat	aac	768
Lys	Asn	Thr	Tyr	Ala	Leu	Val	Val	Ser	Thr	Glu	Asn	Ile	Thr	Tyr	Asn	

245	250	255	
att tac gct ggt gat aat agg tcc atg atg gtt tca aat tgc ttg ttc Ile Tyr Ala Gly Asp Asn Arg Ser Met Met Val Ser Asn Cys Leu Phe 260 265 270			816
cgt gtt ggt ggg gcc gct att ttg ctc tcc aac aag cct gga gat cgt Arg Val Gly Gly Ala Ala Ile Leu Leu Ser Asn Lys Pro Gly Asp Arg 275 280 285			864
aga cgg tcc aag tac gag cta gtt cac acg gtt cga acg cat acc gga Arg Arg Ser Lys Tyr Glu Leu Val His Thr Val Arg Thr His Thr Gly 290 295 300			912
gct gac gac aag tct ttt cgt tgc gtg caa caa gga gac gat gag aac Ala Asp Asp Lys Ser Phe Arg Cys Val Gln Gln Gly Asp Asp Glu Asn 305 310 315 320			960
ggc aaa atc gga gtg agt ttg tcc aag gac ata acc gat gtt gct ggt Gly Lys Ile Gly Val Ser Leu Ser Lys Asp Ile Thr Asp Val Ala Gly 325 330 335			1008
cga acg gtt aag aaa aac ata gca acg ttg ggt ccg ttg att ctt ccg Arg Thr Val Lys Lys Asn Ile Ala Thr Leu Gly Pro Leu Ile Leu Pro 340 345 350			1056
tta agc gag aaa ctt ctt ttt ttc gtt acc ttc atg ggc aag aaa ctt Leu Ser Glu Lys Leu Leu Phe Phe Val Thr Phe Met Gly Lys Lys Leu 355 360 365			1104
ttc aaa gat aaa atc aaa cat tac tac gtc ccg gat ttc aaa ctt gct Phe Lys Asp Lys Ile Lys His Tyr Tyr Val Pro Asp Phe Lys Leu Ala 370 375 380			1152
att gac cat ttt tgt ata cat gcc gga ggc aga gcc gtg att gat gtg Ile Asp His Phe Cys Ile His Ala Gly Gly Arg Ala Val Ile Asp Val 385 390 395 400			1200
cta gag aag aac cta gcc cta gca ccg atc gat gta gag gca tca aga Leu Glu Lys Asn Leu Ala Leu Ala Pro Ile Asp Val Glu Ala Ser Arg 405 410 415			1248
tca acg tta cat aga ttt gga aac act tca tct agc tca ata tgg tat Ser Thr Leu His Arg Phe Gly Asn Thr Ser Ser Ser Ser Ile Trp Tyr 420 425 430			1296
gag ttg gca tac ata gaa gca aaa gga agg atg aag aaa ggt aat aaa Glu Leu Ala Tyr Ile Glu Ala Lys Gly Arg Met Lys Lys Gly Asn Lys 435 440 445			1344
gtt tgg cag att gct tta ggg tca ggc ttt aag tgt aac agt gca gtt Val Trp Gln Ile Ala Leu Gly Ser Gly Phe Lys Cys Asn Ser Ala Val 450 455 460			1392
tgg gtg gct cta aac aat gtc aaa gct tgc aca aat agt cct tgg gaa Trp Val Ala Leu Asn Asn Val Lys Ala Ser Thr Asn Ser Pro Trp Glu 465 470 475 480			1440

cac tgc atc gac aga tac ccg gtc aaa att gat tct gat tca ggt aag 1488
 His Cys Ile Asp Arg Tyr Pro Val Lys Ile Asp Ser Asp Ser Gly Lys
 485 490 495

tca gag act cgt gtc caa aac ggt cgg tcc taa 1521
 Ser Glu Thr Arg Val Gln Asn Gly Arg Ser
 500 505

<210> 38
 <211> 506
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 5' 254 amino acids from A. thaliana FAE1 (SEQ ID
 NO:2) and 3' 252 amino acids from B. napus
 elongase KCS (SEQ ID NO:4) having a mutation at
 residue 307; designated At254 G307D; hypothetical

<400> 38
 Met Thr Ser Val Asn Val Lys Leu Leu Tyr Arg Tyr Val Leu Thr Asn
 1 5 10 15
 Phe Phe Asn Leu Cys Leu Phe Pro Leu Thr Ala Phe Leu Ala Gly Lys
 20 25 30
 Ala Ser Arg Leu Thr Ile Asn Asp Leu His Asn Phe Leu Ser Tyr Leu
 35 40 45
 Gln His Asn Leu Ile Thr Val Thr Leu Leu Phe Ala Phe Thr Val Phe
 50 55 60
 Gly Leu Val Leu Tyr Ile Val Thr Arg Pro Asn Pro Val Tyr Leu Val
 65 70 75 80
 Asp Tyr Ser Cys Tyr Leu Pro Pro Pro His Leu Lys Val Ser Val Ser
 85 90 95
 Lys Val Met Asp Ile Phe Tyr Gln Ile Arg Lys Ala Asp Thr Ser Ser
 100 105 110
 Arg Asn Val Ala Cys Asp Asp Pro Ser Ser Leu Asp Phe Leu Arg Lys
 115 120 125
 Ile Gln Glu Arg Ser Gly Leu Gly Asp Glu Thr Tyr Ser Pro Glu Gly
 130 135 140
 Leu Ile His Val Pro Pro Arg Lys Thr Phe Ala Ala Ser Arg Glu Glu
 145 150 155 160
 Thr Glu Lys Val Ile Ile Gly Ala Leu Glu Asn Leu Phe Glu Asn Thr
 165 170 175
 Lys Val Asn Pro Arg Glu Ile Gly Ile Leu Val Val Asn Ser Ser Met
 180 185 190
 Phe Asn Pro Thr Pro Ser Leu Ser Ala Met Val Val Asn Thr Phe Lys
 195 200 205
 Leu Arg Ser Asn Ile Lys Ser Phe Asn Leu Gly Gly Met Gly Cys Ser
 210 215 220
 Ala Gly Val Ile Ala Ile Asp Leu Ala Lys Asp Leu Leu His Val His
 225 230 235 240
 Lys Asn Thr Tyr Ala Leu Val Val Ser Thr Glu Asn Ile Thr Tyr Asn
 245 250 255
 Ile Tyr Ala Gly Asp Asn Arg Ser Met Met Val Ser Asn Cys Leu Phe
 260 265 270
 Arg Val Gly Gly Ala Ala Ile Leu Leu Ser Asn Lys Pro Gly Asp Arg

275	280	285
Arg Arg Ser Lys Tyr Glu	Leu Val His Thr Val	Arg Thr His Thr Gly
290	295	300
Ala Asp Asp Lys Ser Phe	Arg Cys Val Gln Gln	Gly Asp Asp Glu Asn
305	310	315
Gly Lys Ile Gly Val Ser	Leu Ser Lys Asp Ile	Thr Asp Val Ala Gly
325	330	335
Arg Thr Val Lys Lys Asn	Ile Ala Thr Leu Gly	Pro Leu Ile Leu Pro
340	345	350
Leu Ser Glu Lys Leu Leu	Phe Phe Val Thr Phe	Met Gly Lys Lys Leu
355	360	365
Phe Lys Asp Lys Ile Lys	His Tyr Tyr Val Pro	Asp Phe Lys Leu Ala
370	375	380
Ile Asp His Phe Cys Ile	His Ala Gly Gly Arg	Ala Val Ile Asp Val
385	390	395
Leu Glu Lys Asn Leu Ala	Leu Ala Pro Ile Asp	Val Glu Ala Ser Arg
405	410	415
Ser Thr Leu His Arg Phe	Gly Asn Thr Ser Ser	Ser Ser Ile Trp Tyr
420	425	430
Glu Leu Ala Tyr Ile Glu	Ala Lys Gly Arg Met	Lys Lys Gly Asn Lys
435	440	445
Val Trp Gln Ile Ala Leu	Gly Ser Gly Phe Lys	Cys Asn Ser Ala Val
450	455	460
Trp Val Ala Leu Asn Asn	Val Lys Ala Ser Thr	Asn Ser Pro Trp Glu
465	470	475
His Cys Ile Asp Arg Tyr	Pro Val Lys Ile Asp	Ser Asp Ser Gly Lys
485	490	495
Ser Glu Thr Arg Val Gln	Asn Gly Arg Ser	
500	505	

<210> 39

<211> 1521

<212> DNA

<213> Artificial Sequence

<220>

<223> 5' 519 bp from A. thaliana FAE1 (SEQ ID NO:1) and
 3' 1002 bp from B. napus elongase KCS (SEQ ID
 NO:3) and having a mutation at position 920;
 designated At173 G307D

<221> CDS

<222> (1)...(1518)

<400> 39

atg acg tcc gtt aac gtt aag ctc ctt tac cgt tac gtc tta acc aac	48
Met Thr Ser Val Asn Val Lys Leu Leu Tyr Arg Tyr Val Leu Thr Asn	
1 5 10 15	

ttt ttc aac ctc tgt ttg ttc ccg tta acg gcg ttc ctc gcc gga aaa	96
Phe Phe Asn Leu Cys Leu Phe Pro Leu Thr Ala Phe Leu Ala Gly Lys	
20 25 30	

gcc tct cgg ctt acc ata aac gat ctc cac aac ttc ctt tcc tat ctc	144
Ala Ser Arg Leu Thr Ile Asn Asp Leu His Asn Phe Leu Ser Tyr Leu	
35 40 45	

caa cac aac ctt ata aca gta act tta ctc ttt gct ttc act gtt ttc	192
Gln His Asn Leu Ile Thr Val Thr Leu Leu Phe Ala Phe Thr Val Phe	
50 55 60	
ggt ttg gtt ctc tac atc gta acc cga ccc aat ccg gtt tat ctc gtt	240
Gly Leu Val Leu Tyr Ile Val Thr Arg Pro Asn Pro Val Tyr Leu Val	
65 70 75 80	
gac tac tcg tgt tac ctt cca cca ccg cat ctc aaa gtt agt gtc tct	288
Asp Tyr Ser Cys Tyr Leu Pro Pro Pro His Leu Lys Val Ser Val Ser	
85 90 95	
aaa gtc atg gat att ttc tac caa ata aga aaa gct gat act tct tca	336
Lys Val Met Asp Ile Phe Tyr Gln Ile Arg Lys Ala Asp Thr Ser Ser	
100 105 110	
cgg aac gtg gca tgt gat gat ccg tcc tcg ctc gat ttc ctg agg aag	384
Arg Asn Val Ala Cys Asp Asp Pro Ser Ser Leu Asp Phe Leu Arg Lys	
115 120 125	
att caa gag cgt tca ggt cta ggt gat gag acg tac agt cct gag gga	432
Ile Gln Glu Arg Ser Gly Leu Gly Asp Glu Thr Tyr Ser Pro Glu Gly	
130 135 140	
ctc att cac gta cca ccg cgg aag act ttt gca gcg tca cgt gaa gag	480
Leu Ile His Val Pro Pro Arg Lys Thr Phe Ala Ala Ser Arg Glu Glu	
145 150 155 160	
aca gag aag gtt atc atc ggt gcg ctc gaa aat cta ttc aag aac acc	528
Thr Glu Lys Val Ile Ile Gly Ala Leu Glu Asn Leu Phe Lys Asn Thr	
165 170 175	
aac gtt aac cct aaa gat ata ggt ata ctt gtg gtg aac tca agc atg	576
Asn Val Asn Pro Lys Asp Ile Gly Ile Leu Val Val Asn Ser Ser Met	
180 185 190	
ttt aat cca act cca tcg ctc tcc gcg atg gtc gtt aac act ttc aag	624
Phe Asn Pro Thr Pro Ser Leu Ser Ala Met Val Val Asn Thr Phe Lys	
195 200 205	
ctc cga agc aac gta aga agc ttt aac ctt ggt ggc atg ggt tgt agt	672
Leu Arg Ser Asn Val Arg Ser Phe Asn Leu Gly Gly Met Gly Cys Ser	
210 215 220	
gcc gcc gtt ata gcc att gat cta gca aag gac ttg ttg cat gtc cat	720
Ala Gly Val Ile Ala Ile Asp Leu Ala Lys Asp Leu Leu His Val His	
225 230 235 240	
aaa aat acg tat gct ctt gtg gtg agc aca gag aac atc act tat aac	768
Lys Asn Thr Tyr Ala Leu Val Val Ser Thr Glu Asn Ile Thr Tyr Asn	
245 250 255	
att tac gct ggt gat aat agg tcc atg atg gtt tca aat tgc ttg ttc	816
Ile Tyr Ala Gly Asp Asn Arg Ser Met Met Val Ser Asn Cys Leu Phe	
260 265 270	
cgt gtt ggt ggg gcc gct att ttg ctc tcc aac aag cct gga gat cgt	864

Arg	Val	Gly	Gly	Ala	Ala	Ile	Leu	Leu	Ser	Asn	Lys	Pro	Gly	Asp	Arg	
		275					280					285				
aga	cgg	tcc	aag	tac	gag	cta	gtt	cac	acg	gtt	cga	acg	cat	acc	gga	912
Arg	Arg	Ser	Lys	Tyr	Glu	Leu	Val	His	Thr	Val	Arg	Thr	His	Thr	Gly	
		290				295					300					
gct	gac	gac	aag	tct	ttt	cgt	tgc	gtg	caa	caa	gga	gac	gat	gag	aac	960
Ala	Asp	Asp	Lys	Ser	Phe	Arg	Cys	Val	Gln	Gln	Gly	Asp	Asp	Glu	Asn	
305					310					315					320	
ggc	aaa	atc	gga	gtg	agt	ttg	tcc	aag	gac	ata	acc	gat	gtt	gct	ggc	1008
Gly	Lys	Ile	Gly	Val	Ser	Leu	Ser	Lys	Asp	Ile	Thr	Asp	Val	Ala	Gly	
				325					330					335		
cga	acg	gtt	aag	aaa	aac	ata	gca	acg	ttg	ggc	ccg	ttg	att	ctt	ccg	1056
Arg	Thr	Val	Lys	Lys	Asn	Ile	Ala	Thr	Leu	Gly	Pro	Leu	Ile	Leu	Pro	
			340					345					350			
tta	agc	gag	aaa	ctt	ctt	ttt	ttc	gtt	acc	ttc	atg	ggc	aag	aaa	ctt	1104
Leu	Ser	Glu	Lys	Leu	Leu	Phe	Phe	Val	Thr	Phe	Met	Gly	Lys	Lys	Leu	
		355					360					365				
ttc	aaa	gat	aaa	atc	aaa	cat	tac	tac	gtc	ccg	gat	ttc	aaa	ctt	gct	1152
Phe	Lys	Asp	Lys	Ile	Lys	His	Tyr	Tyr	Val	Pro	Asp	Phe	Lys	Leu	Ala	
	370					375					380					
att	gac	cat	ttt	tgt	ata	cat	gcc	gga	ggc	aga	gcc	gtg	att	gat	gtg	1200
Ile	Asp	His	Phe	Cys	Ile	His	Ala	Gly	Gly	Arg	Ala	Val	Ile	Asp	Val	
385					390					395					400	
cta	gag	aag	aac	cta	gcc	cta	gca	ccg	atc	gat	gta	gag	gca	tca	aga	1248
Leu	Glu	Lys	Asn	Leu	Ala	Leu	Ala	Pro	Ile	Asp	Val	Glu	Ala	Ser	Arg	
			405						410					415		
tca	acg	tta	cat	aga	ttt	gga	aac	act	tca	tct	agc	tca	ata	tgg	tat	1296
Ser	Thr	Leu	His	Arg	Phe	Gly	Asn	Thr	Ser	Ser	Ser	Ser	Ile	Trp	Tyr	
			420					425					430			
gag	ttg	gca	tac	ata	gaa	gca	aaa	gga	agg	atg	aag	aaa	ggc	aat	aaa	1344
Glu	Leu	Ala	Tyr	Ile	Glu	Ala	Lys	Gly	Arg	Met	Lys	Lys	Gly	Asn	Lys	
		435					440					445				
gtt	tgg	cag	att	gct	tta	ggg	tca	ggc	ttt	aag	tgt	aac	agt	gca	gtt	1392
Val	Trp	Gln	Ile	Ala	Leu	Gly	Ser	Gly	Phe	Lys	Cys	Asn	Ser	Ala	Val	
	450					455					460					
tgg	gtg	gct	cta	aac	aat	gtc	aaa	gct	tcg	aca	aat	agt	cct	tgg	gaa	1440
Trp	Val	Ala	Leu	Asn	Asn	Val	Lys	Ala	Ser	Thr	Asn	Ser	Pro	Trp	Glu	
465					470					475					480	
cac	tgc	atc	gac	aga	tac	ccg	gtc	aaa	att	gat	tct	gat	tca	ggc	aag	

500

505

<210> 40
 <211> 506
 <212> PRT
 <213> Artificial Sequence

<220>

<223> 5' 173 amino acids from *A. thaliana* FAE1 (SEQ ID NO:2) and 3' 333 amino acids from *B. napus* elongase KCS (SEQ ID NO:4) having a mutation at residue 307; designated At173 G307D; hypothetical

<400> 40

Met	Thr	Ser	Val	Asn	Val	Lys	Leu	Leu	Tyr	Arg	Tyr	Val	Leu	Thr	Asn
1				5					10					15	
Phe	Phe	Asn	Leu	Cys	Leu	Phe	Pro	Leu	Thr	Ala	Phe	Leu	Ala	Gly	Lys
			20					25					30		
Ala	Ser	Arg	Leu	Thr	Ile	Asn	Asp	Leu	His	Asn	Phe	Leu	Ser	Tyr	Leu
			35				40					45			
Gln	His	Asn	Leu	Ile	Thr	Val	Thr	Leu	Leu	Phe	Ala	Phe	Thr	Val	Phe
	50					55					60				
Gly	Leu	Val	Leu	Tyr	Ile	Val	Thr	Arg	Pro	Asn	Pro	Val	Tyr	Leu	Val
65					70					75					80
Asp	Tyr	Ser	Cys	Tyr	Leu	Pro	Pro	Pro	His	Leu	Lys	Val	Ser	Val	Ser
				85					90					95	
Lys	Val	Met	Asp	Ile	Phe	Tyr	Gln	Ile	Arg	Lys	Ala	Asp	Thr	Ser	Ser
			100					105					110		
Arg	Asn	Val	Ala	Cys	Asp	Asp	Pro	Ser	Ser	Leu	Asp	Phe	Leu	Arg	Lys
			115				120					125			
Ile	Gln	Glu	Arg	Ser	Gly	Leu	Gly	Asp	Glu	Thr	Tyr	Ser	Pro	Glu	Gly
	130					135					140				
Leu	Ile	His	Val	Pro	Pro	Arg	Lys	Thr	Phe	Ala	Ala	Ser	Arg	Glu	Glu
145						150				155					160
Thr	Glu	Lys	Val	Ile	Ile	Gly	Ala	Leu	Glu	Asn	Leu	Phe	Lys	Asn	Thr
				165					170					175	
Asn	Val	Asn	Pro	Lys	Asp	Ile	Gly	Ile	Leu	Val	Val	Asn	Ser	Ser	Met
			180				185						190		
Phe	Asn	Pro	Thr	Pro	Ser	Leu	Ser	Ala	Met	Val	Val	Asn	Thr	Phe	Lys
		195				200						205			
Leu	Arg	Ser	Asn	Val	Arg	Ser	Phe	Asn	Leu	Gly	Gly	Met	Gly	Cys	Ser
	210					215					220				
Ala	Gly	Val	Ile	Ala	Ile	Asp	Leu	Ala	Lys	Asp	Leu	Leu	His	Val	His
225					230					235					240
Lys	Asn	Thr	Tyr	Ala	Leu	Val	Val	Ser	Thr	Glu	Asn	Ile	Thr	Tyr	Asn
				245						250				255	
Ile	Tyr	Ala	Gly	Asp	Asn	Arg	Ser	Met	Met	Val	Ser	Asn	Cys	Leu	Phe
			260					265					270		
Arg	Val	Gly	Gly	Ala	Ala	Ile	Leu	Leu	Ser	Asn	Lys	Pro	Gly	Asp	Arg
		275				280						285			
Arg	Arg	Ser	Lys	Tyr	Glu	Leu	Val	His	Thr	Val	Arg	Thr	His	Thr	Gly
	290					295					300				
Ala	Asp	Asp	Lys	Ser	Phe	Arg	Cys	Val	Gln	Gln	Gly	Asp	Asp	Glu	Asn
305					310					315					320
Gly	Lys	Ile	Gly	Val	Ser	Leu	Ser	Lys	Asp	Ile	Thr	Asp	Val	Ala	Gly
				325					330					335	

Arg Thr Val Lys Lys Asn Ile Ala Thr Leu Gly Pro Leu Ile Leu Pro
 340 345 350
 Leu Ser Glu Lys Leu Leu Phe Phe Val Thr Phe Met Gly Lys Lys Leu
 355 360 365
 Phe Lys Asp Lys Ile Lys His Tyr Tyr Val Pro Asp Phe Lys Leu Ala
 370 375 380
 Ile Asp His Phe Cys Ile His Ala Gly Gly Arg Ala Val Ile Asp Val
 385 390 395 400
 Leu Glu Lys Asn Leu Ala Leu Ala Pro Ile Asp Val Glu Ala Ser Arg
 405 410 415
 Ser Thr Leu His Arg Phe Gly Asn Thr Ser Ser Ser Ser Ile Trp Tyr
 420 425 430
 Glu Leu Ala Tyr Ile Glu Ala Lys Gly Arg Met Lys Lys Gly Asn Lys
 435 440 445
 Val Trp Gln Ile Ala Leu Gly Ser Gly Phe Lys Cys Asn Ser Ala Val
 450 455 460
 Trp Val Ala Leu Asn Asn Val Lys Ala Ser Thr Asn Ser Pro Trp Glu
 465 470 475 480
 His Cys Ile Asp Arg Tyr Pro Val Lys Ile Asp Ser Asp Ser Gly Lys
 485 490 495
 Ser Glu Thr Arg Val Gln Asn Gly Arg Ser
 500 505

<210> 41

<211> 1521

<212> DNA

<213> Artificial Sequence

<220>

<223> 5' 1197 bp from B. napus elongase KCS (SEQ ID
 NO:3) and 3' 324 bp from A. thaliana FAE1 (SEQ ID
 NO:1) and having a mutation at nucleotide position
 920; designated Bn399 G307D; hypothetical

<221> CDS

<222> (1)...(1518)

<400> 41

atg acg tcc att aac gtt aag ctc ctt tac cat tac gtc ata acc aac	48
Met Thr Ser Ile Asn Val Lys Leu Leu Tyr His Tyr Val Ile Thr Asn	
1 5 10 15	
ctt ttc aac ctt tgc ttc ttt ccg tta acg gcg atc gtc gcc gga aaa	96
Leu Phe Asn Leu Cys Phe Phe Pro Leu Thr Ala Ile Val Ala Gly Lys	
20 25 30	
gcc tat cgg ctt acc ata gac gat ctt cac cac tta tac tat tcc tat	144
Ala Tyr Arg Leu Thr Ile Asp Asp Leu His His Leu Tyr Tyr Ser Tyr	
35 40 45	
ctc caa cac aac ctc ata acc atc gct cca ctc ttt gcc ttc acc gtt	192
Leu Gln His Asn Leu Ile Thr Ile Ala Pro Leu Phe Ala Phe Thr Val	
50 55 60	
ttc ggt tgc gtt ctc tac atc gca acc cgg ccc aaa ccg gtt tac ctc	240
Phe Gly Ser Val Leu Tyr Ile Ala Thr Arg Pro Lys Pro Val Tyr Leu	
65 70 75 80	

	0	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	
0	0	1	4	9	16	25	36	49	64	81	100	121	144	169	196	225	256	289	324	361	400	441	484	529	576	625	676	729	784	841	900	961	1024	1089	1156	1225	1296	1369	1444	1521	1600	1681	1764	1849	1936	2025	2116	2209	2304	2401	2500	2601	2704	2809	2916	3025	3136	3249	3364	3481	3600	3721	3844	3969	4096	4225	4356	4489	4624	4761	4900	5041	5184	5329	5476	5625	5776	5929	6084	6241	6400	6561	6724	6889	7056	7225	7396	7569	7744	7921	8100	8281	8464	8649	8836	9025	9216	9409	9604	9801	10000

gct gac gac aag tct ttt cgt tgc gtg caa caa gga gac gat gag aac	960
Ala Asp Asp Lys Ser Phe Arg Cys Val Gln Gln Gly Asp Asp Glu Asn	
305 310 315 320	
ggc aaa atc gga gtg agt ttg tcc aag gac ata acc gat gtt gct ggt	1008
Gly Lys Ile Gly Val Ser Leu Ser Lys Asp Ile Thr Asp Val Ala Gly	
325 330 335	
cga acg gtt aag aaa aac ata gca acg ttg ggt ccg ttg att ctt ccg	1056
Arg Thr Val Lys Lys Asn Ile Ala Thr Leu Gly Pro Leu Ile Leu Pro	
340 345 350	
tta agc gag aaa ctt ctt ttt ttc gtt acc ttc atg ggc aag aaa ctt	1104
Leu Ser Glu Lys Leu Leu Phe Phe Val Thr Phe Met Gly Lys Lys Leu	
355 360 365	
ttc aaa gat aaa atc aaa cat tac tac gtc ccg gat ttc aaa ctt gct	1152
Phe Lys Asp Lys Ile Lys His Tyr Tyr Val Pro Asp Phe Lys Leu Ala	
370 375 380	
att gac cat ttt tgt ata cat gcc gga ggc aga gcc gtg atc gat gag	1200
Ile Asp His Phe Cys Ile His Ala Gly Gly Arg Ala Val Ile Asp Glu	
385 390 395 400	
cta gag aag aac tta gga cta tcg ccg atc gat gtg gag gca tct aga	1248
Leu Glu Lys Asn Leu Gly Leu Ser Pro Ile Asp Val Glu Ala Ser Arg	
405 410 415	
tca acg tta cat aga ttt ggg aat act tca tct agc tca att tgg tat	1296
Ser Thr Leu His Arg Phe Gly Asn Thr Ser Ser Ser Ser Ile Trp Tyr	
420 425 430	
gaa tta gca tac ata gag gca aag gga aga atg aag aaa ggg aat aaa	1344
Glu Leu Ala Tyr Ile Glu Ala Lys Gly Arg Met Lys Lys Gly Asn Lys	
435 440 445	
gct tgg cag att gct tta gga tca ggg ttt aag tgt aat agt gcg gtt	1392
Ala Trp Gln Ile Ala Leu Gly Ser Gly Phe Lys Cys Asn Ser Ala Val	
450 455 460	
tgg gtg gct cta cgc aat gtc aag gca tcg gca aat agt cct tgg caa	1440
Trp Val Ala Leu Arg Asn Val Lys Ala Ser Ala Asn Ser Pro Trp Gln	
465 470 475 480	
cat tgc atc gat aga tat ccg gtt aaa att gat tct gat ttg tca aag	1488
His Cys Ile Asp Arg Tyr Pro Val Lys Ile Asp Ser Asp Leu Ser Lys	
485 490 495	
tca aag act cat gtc caa aac ggt cgg tcc taa	1521
Ser Lys Thr His Val Gln Asn Gly Arg Ser	
500 505	

<210> 42

<211> 506

<212> PRT

<213> Artificial Sequence

<220>

<223> 5' 399 amino acids from *B. napus* elongase KCS (SEQ ID NO:3) and 3' 107 amino acids from *A. thaliana* FAE1 (SEQ ID NO:1) having a mutation at residue 306; designated Bn399 G307D; hypothetical

<400> 42

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		20						25				30			
Ala	Tyr	Arg	Leu	Thr	Ile	Asp	Asp	Leu	His	His	Leu	Tyr	Tyr	Ser	Tyr
	35					40					45				
Leu	Gln	His	Asn	Leu	Ile	Thr	Ile	Ala	Pro	Leu	Phe	Ala	Phe	Thr	Val
50					55					60					
Phe	Gly	Ser	Val	Leu	Tyr	Ile	Ala	Thr	Arg	Pro	Lys	Pro	Val	Tyr	Leu
65				70					75						80
Val	Glu	Tyr	Ser	Cys	Tyr	Leu	Pro	Pro	Thr	His	Cys	Arg	Ser	Ser	Ile
			85					90					95		
Ser	Lys	Val	Met	Asp	Ile	Phe	Tyr	Gln	Val	Arg	Lys	Ala	Asp	Pro	Ser
		100						105					110		
Arg	Asn	Gly	Thr	Cys	Asp	Asp	Ser	Ser	Trp	Leu	Asp	Phe	Leu	Arg	Lys
	115						120					125			
Ile	Gln	Glu	Arg	Ser	Gly	Leu	Gly	Asp	Glu	Thr	His	Gly	Pro	Glu	Gly
130					135					140					
Leu	Leu	Gln	Val	Pro	Pro	Arg	Lys	Thr	Phe	Ala	Ala	Ala	Arg	Glu	Glu
145				150					155						160
Thr	Glu	Gln	Val	Ile	Ile	Gly	Ala	Leu	Glu	Asn	Leu	Phe	Lys	Asn	Thr
			165					170						175	
Asn	Val	Asn	Pro	Lys	Asp	Ile	Gly	Ile	Leu	Val	Val	Asn	Ser	Ser	Met
		180					185					190			
Phe	Asn	Pro	Thr	Pro	Ser	Leu	Ser	Ala	Met	Val	Val	Asn	Thr	Phe	Lys
	195					200						205			
Leu	Arg	Ser	Asn	Val	Arg	Ser	Phe	Asn	Leu	Gly	Gly	Met	Gly	Cys	Ser
	210				215					220					
Ala	Gly	Val	Ile	Ala	Ile	Asp	Leu	Ala	Lys	Asp	Leu	Leu	His	Val	His
225				230						235				240	
Lys	Asn	Thr	Tyr	Ala	Leu	Val	Val	Ser	Thr	Glu	Asn	Ile	Thr	Tyr	Asn
			245					250					255		
Ile	Tyr	Ala	Gly	Asp	Asn	Arg	Ser	Met	Met	Val	Ser	Asn	Cys	Leu	Phe
	260						265						270		
Arg	Val	Gly	Gly	Ala	Ala	Ile	Leu	Leu	Ser	Asn	Lys	Pro	Gly	Asp	Arg
	275						280					285			
Arg	Arg	Ser	Lys	Tyr	Glu	Leu	Val	His	Thr	Val	Arg	Thr	His	Thr	Gly
	290					295				300					
Ala	Asp	Asp	Lys	Ser	Phe	Arg	Cys	Val	Gln	Gln	Gly	Asp	Asp	Glu	Asn
305				310						315				320	
Gly	Lys	Ile	Gly	Val	Ser	Leu	Ser	Lys	Asp	Ile	Thr	Asp	Val	Ala	Gly
			325					330					335		
Arg	Thr	Val	Lys	Lys	Asn	Ile	Ala	Thr	Leu	Gly	Pro	Leu	Ile	Leu	Pro
		340					345					350			
Leu	Ser	Glu	Lys	Leu	Leu	Phe	Phe	Val	Thr	Phe	Met	Gly	Lys	Lys	Leu
	355					360					365				
Phe	Lys	Asp	Lys	Ile	Lys	His	Tyr	Tyr	Val	Pro	Asp	Phe	Lys	Leu	Ala
	370					375					380				
Ile	Asp	His	Phe	Cys	Ile	His	Ala	Gly	Gly	Arg	Ala	Val	Ile	Asp	Glu

385		390		395		400
Leu	Glu	Lys	Asn	Leu	Gly	Leu
				Ser	Pro	Ile
				Asp	Val	Glu
				Ala	Ser	Arg
		405		410		415
Ser	Thr	Leu	His	Arg	Phe	Gly
				Asn	Thr	Ser
				Ser	Ser	Ser
		420		425		430
Glu	Leu	Ala	Tyr	Ile	Glu	Ala
				Lys	Gly	Arg
				Met	Lys	Lys
		435		440		445
Ala	Trp	Gln	Ile	Ala	Leu	Gly
				Ser	Gly	Phe
				Lys	Cys	Asn
		450		455		460
Trp	Val	Ala	Leu	Arg	Asn	Val
				Lys	Ala	Ser
				Ala	Asn	Ser
				Pro	Trp	Gln
		465		470		475
His	Cys	Ile	Asp	Arg	Tyr	Pro
				Val	Lys	Ile
				Asp	Ser	Asp
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Ser	Lys	Thr	His	Val	Gln	Asn
				Gly	Arg	Ser
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<400> 43
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25

<210> 44
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<400> 44
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33

<210> 45
 <211> 28
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28

<210> 46
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28

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<400> 47
cccaaaccgg ttacctcgt tga

23

<210> 48
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<400> 48
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23

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27

<210> 50
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<400> 50
tttagagaca ctaactctgc aatgcgg

27

<210> 51
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<400> 51
ccaccgcac tcagagttag tgtctct

27

<210> 52
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<400> 52
 agagacacta actctgagat gcggtgg 27

<210> 53
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<400> 53
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<210> 54
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<220>
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<400> 54
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<210> 55
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 <212> DNA
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<400> 55
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<210> 56
 <211> 38
 <212> DNA
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<220>
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<400> 56
 ccgaattctt aggaccgacc gttttggaca tgagtctt 38